

Supplementary Table 1: Association of CpG methylation sites with fasting lipoprotein parameters in the discovery and replication samples, for sites which reached genome-wide levels of significance ($P < 1.1 \times 10^{-7}$) in the discovery cohort.

	Marker	Chromosome	Position	Gene	Discovery subsample (N=663)		Replication subsample (N=331)	
					β	P	β	P
<i>HDL parameters</i>								
Concentration of medium particles	cg05670596	3	46448496	<i>CCRL2</i>	-0.001	7.9*10 ⁻⁸	8.4*10 ⁻⁵	0.80
Concentration of small particles	cg23631932	8	52322341	<i>PXDNL</i>	-0.001	8.3*10 ⁻⁸	-0.0001	0.55
<i>LDL parameters</i>								
Concentration of large particles	cg00574958	11	68607622	<i>CPT1A</i>	2.1*10 ⁻⁵	2.5*10 ⁻⁸	1.2*10 ⁻⁵	0.01
Concentration of small particles	cg00574958	11	68607622	<i>CPT1A</i>	-1.3*10 ⁻⁵	7.1*10 ⁻¹³	-1.1*10 ⁻⁵	1.4*10 ⁻⁵
Total particles	cg00574958	11	68607622	<i>CPT1A</i>	-1.3*10 ⁻⁵	2.3*10 ⁻⁹	-1.2	0.0001
Average diameter	cg00574958	11	68607622	<i>CPT1A</i>	0.01	4.9*10 ⁻¹³	0.01	6.5*10 ⁻⁶
	cg06500161	21	43656587	<i>ABCG1</i>	-0.01	3.9*10 ⁻⁸	-0.005	0.03
<i>VLDL parameters</i>								
Concentration of large particles	cg00574958	11	68607622	<i>CPT1A</i>	-0.001	1.5*10 ⁻¹²	-0.001	1.6*10 ⁻⁵
	cg17058475	11	68607737	<i>CPT1A</i>	-0.001	1.8*10 ⁻⁷	-0.001	0.0001
Concentration of medium particles	cg00574958	11	68607622	<i>CPT1A</i>	-0.0002	8.0*10 ⁻¹⁵	-0.0002	0.0002
	cg17058475	11	68607737	<i>CPT1A</i>	-0.0003	2.6*10 ⁻¹¹	-0.0002	1.4*10 ⁻⁵
	cg09737197	11	68607675	<i>CPT1A</i>	-0.0002	3.2*10 ⁻⁷	-0.0002	0.01
Total particles	cg00574958	11	68607622	<i>CPT1A</i>	-0.0002	4.3*10 ⁻¹⁶	-0.0001	5.4*10 ⁻⁵
	cg17058475	11	68607737	<i>CPT1A</i>	-0.0002	4.2*10 ⁻¹¹	-0.0002	8.4*10 ⁻⁵
Average diameter	cg17545182	1	2.48E+08	<i>OR2C3;LOC148</i>	-0.003	1.8*10 ⁻⁸	0.0002	0.68

Supplementary Table 2: Association of CpG methylation sites with fasting lipoprotein parameters in the discovery and replication samples, for sites which reached genome-wide levels of significance ($P < 1.1 \times 10^{-7}$) in the discovery cohort, and replicated at a Bonferroni corrected alpha of .05 ($P < .004$) in the replication cohort, in models with controlled for age, gender, data collection center and BMI (model 1) or fasting insulin (model 2).

Marker	Discovery subsample (N=668)				Replication subsample (N=331)			
	Model1		Model2		Model1		Model2	
	β	P	β	P	β	P	β	P
LDL parameters								
Concentration of small particles	cg00574958	-1.3*10 ⁻⁵	5.2*10 ⁻¹³	-1.1*10 ⁻⁵	9.2*10 ⁻¹⁰	-1.1*10 ⁻⁵	1.5*10 ⁻⁵	-9.2*10 ⁻⁶
Total particles	cg00574958	-1.3*10 ⁻⁵	3.6*10 ⁻⁹	-1.2*10 ⁻⁵	2.7*10 ⁻⁷	-1.1*10 ⁻⁵	0.0001	-1.0*10 ⁻⁵
Average diameter	cg00574958	0.01	1.2*10 ⁻¹³	0.01	1.2*10 ⁻⁹	0.01	4.1*10 ⁻⁶	0.01
VLDL parameters								
Concentration of large particles	cg00574958	-0.001	2.0*10 ⁻¹²	-0.001	2.4*10 ⁻⁹	-0.001	3.1*10 ⁻⁵	-0.001
	cg17058475	-0.001	2.9*10 ⁻⁷	-0.001	1.1*10 ⁻⁵	-0.001	0.0002	-0.001
Concentration of medium particles	cg00574958	-0.0002	2.0*10 ⁻¹⁴	-0.0002	2.0*10 ⁻¹²	-0.0002	0.0002	-0.0001
	cg17058475	-0.0002	8.3*10 ⁻¹¹	-0.0002	9.6*10 ⁻¹⁰	-0.0002	1.8*10 ⁻⁵	-0.0002
Total particles	cg00574958	-0.0002	1.1*10 ⁻¹⁵	-0.0002	3.1*10 ⁻¹³	-0.0001	5.6*10 ⁻⁵	-0.000
	cg17058475	-1.8*10 ⁻⁴	9.6*10 ⁻¹¹	-0.0002	2.6*10 ⁻⁹	-0.0002	1.1*10 ⁻⁵	-0.0002
								3.3*10 ⁻⁵

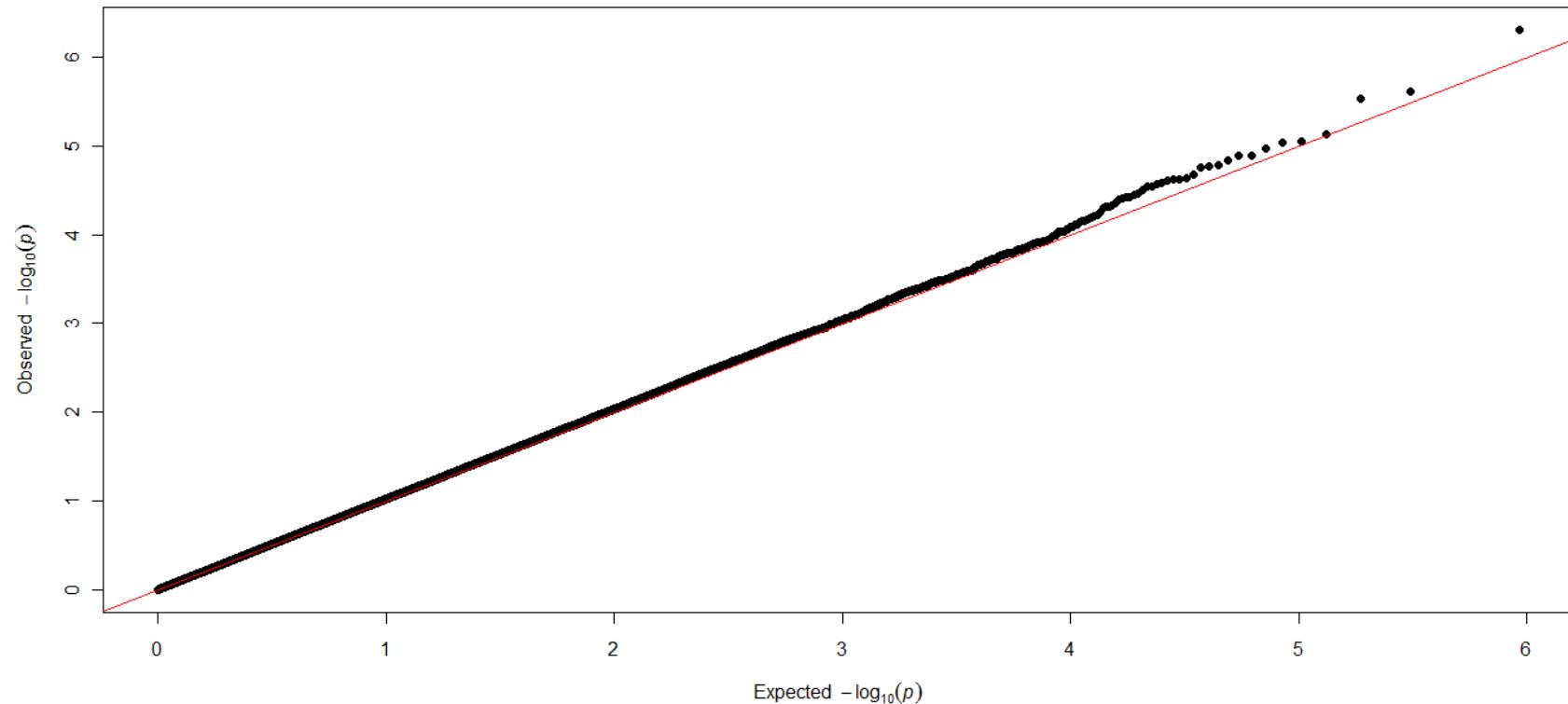
Supplementary Table 3: Coefficients of genomic control (λ) for the genome-wide analysis of CpG methylation sites with fasting lipoprotein parameters in the discovery sample

<i>Measure</i>	λ
<i>HDL parameters</i>	
Concentration of large particles, nmol/L	1.0
Concentration of medium particles, nmol/L	1.1
Concentration of small particles, nmol/L	1.2
Total particles, nmol/L	1.1
Average diameter, nm	1.0
<i>LDL parameters</i>	
Concentration of large particles, nmol/L	1.0
Concentration of small particles, nmol/L	1.0
Total particles, nmol/L	1.0
Average diameter, nm	1.0
<i>IDL parameters</i>	
Total particles, nmol/L	1.0
<i>VLDL parameters</i>	

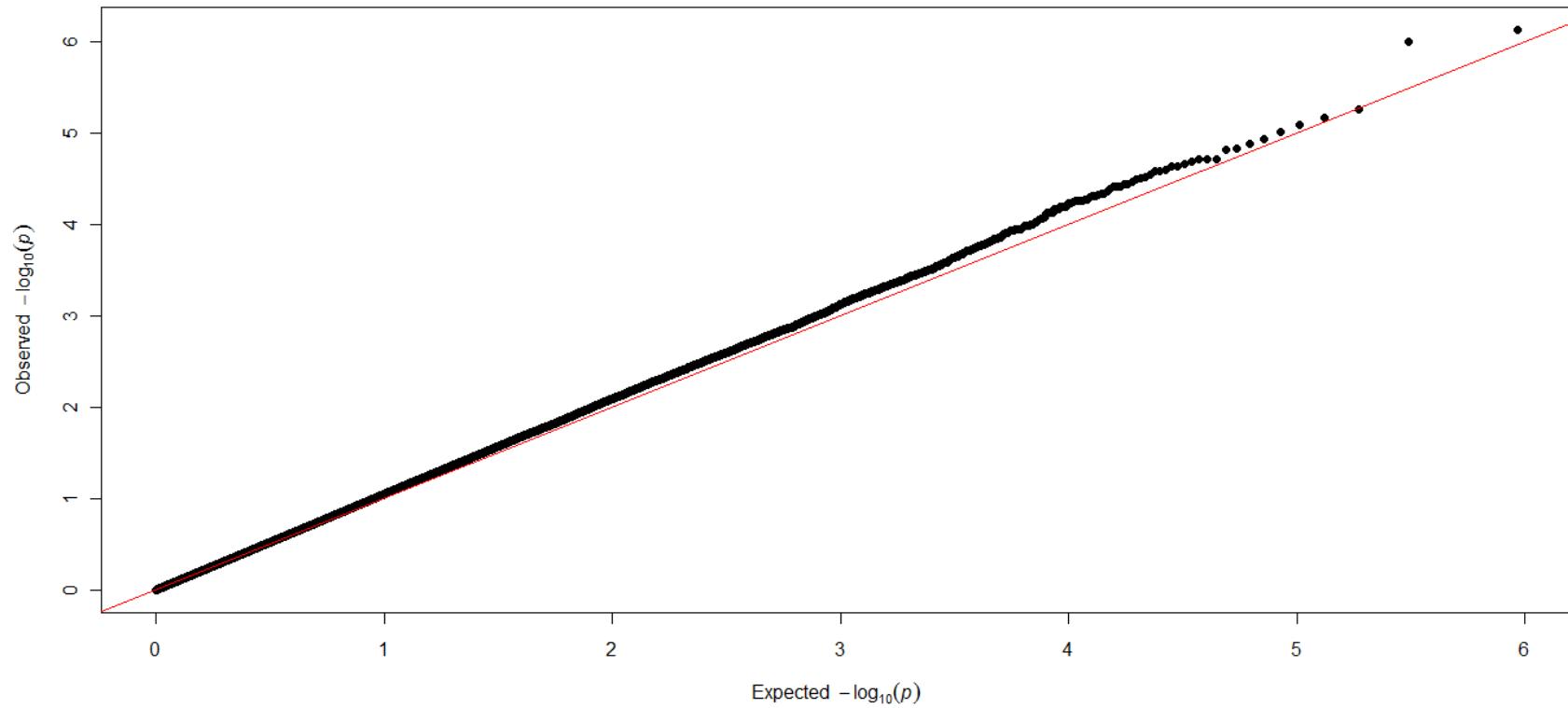
Concentration of large particles, nmol/L	1.0
Concentration of medium particles, nmol/L	1.0
Concentration of small particles, nmol/L	1.1
Total particles, nmol/L	1.0
Average diameter, nm	1.2

Supplementary Figure 1: Quartile-Quartile plots for the epigenome-wide analysis of methylation status at CpG sites with fasting lipoprotein parameters (discovery subsample, n=663).

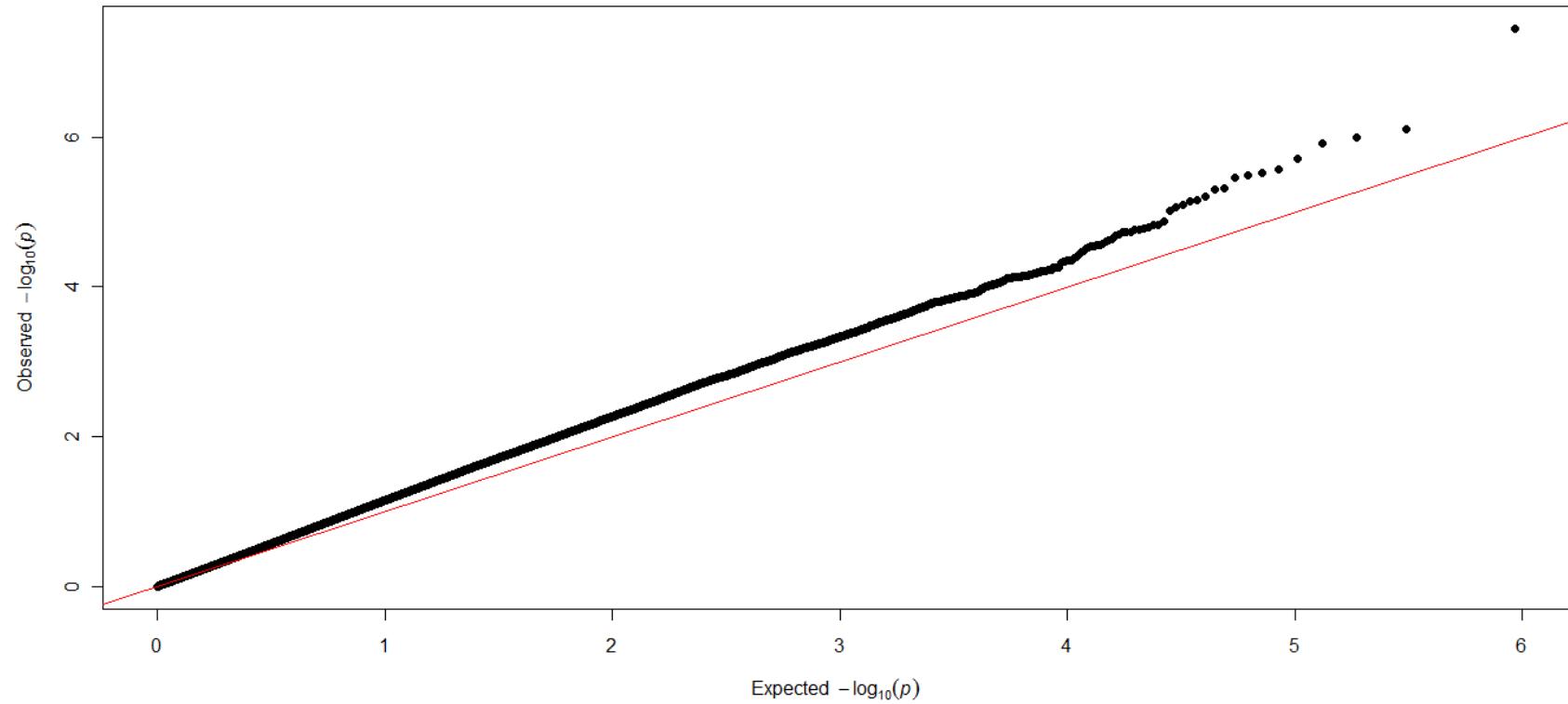
Panel A: Concentration of large HDL particles ($\lambda=1.0$)



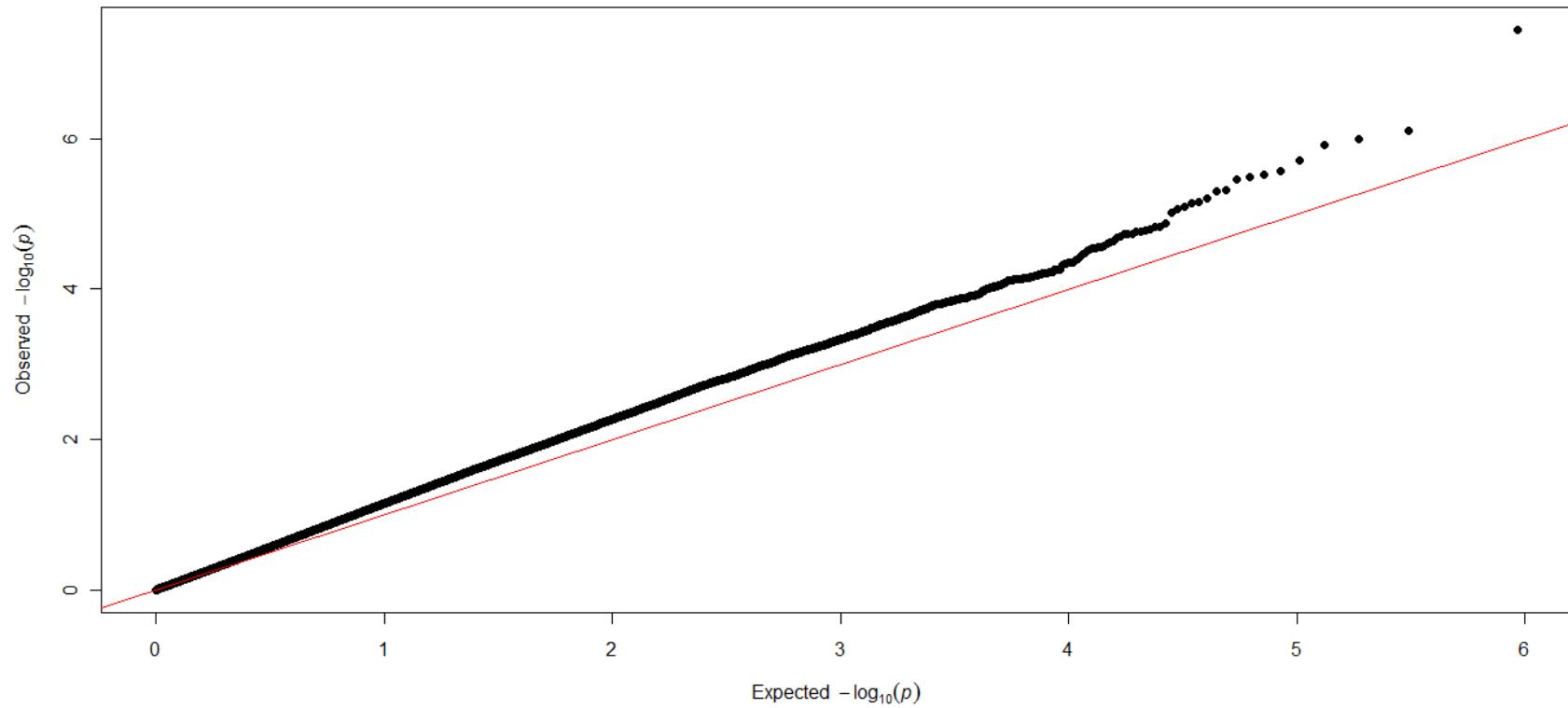
Panel B: Concentration of medium HDL particles ($\lambda=1.1$)



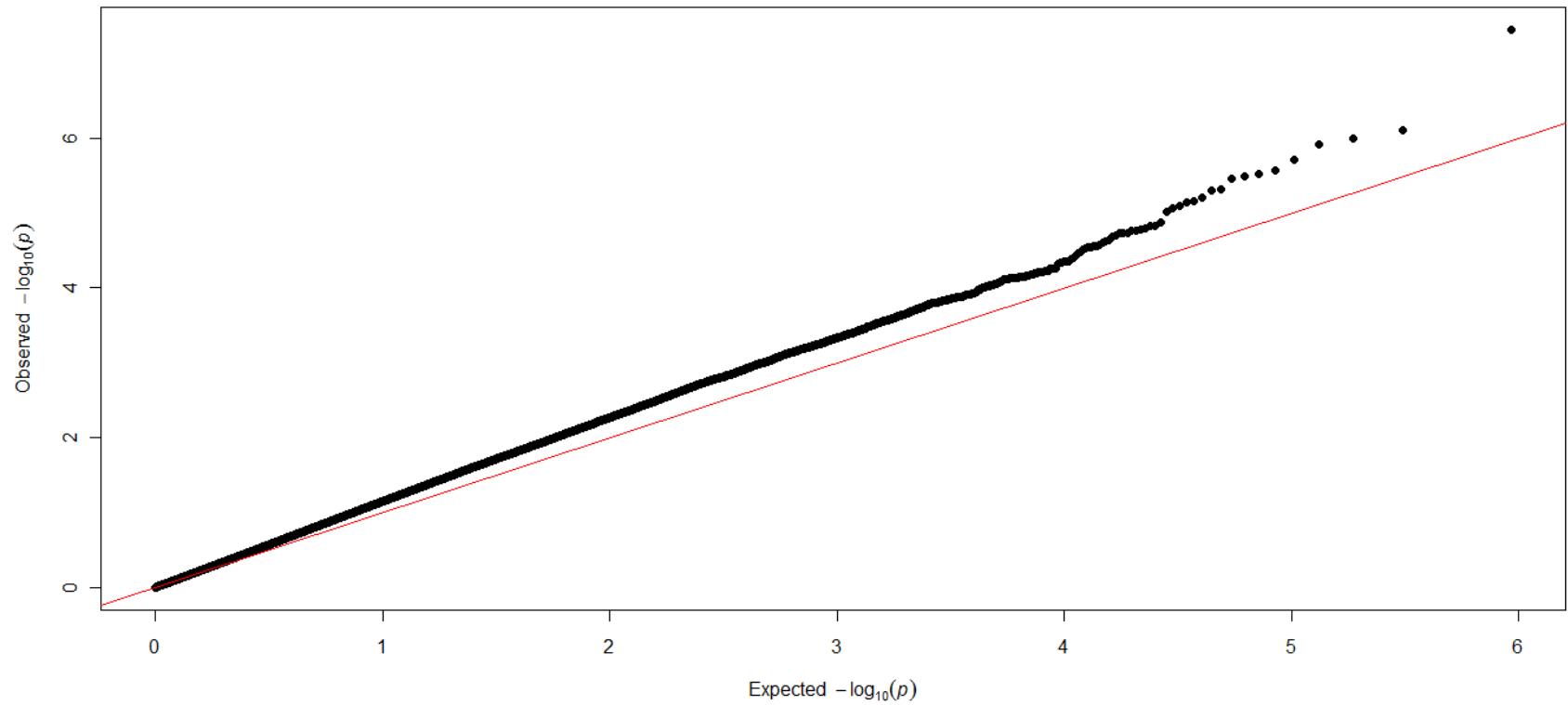
Panel C: Concentration of small HDL particles ($\lambda=1.2$)



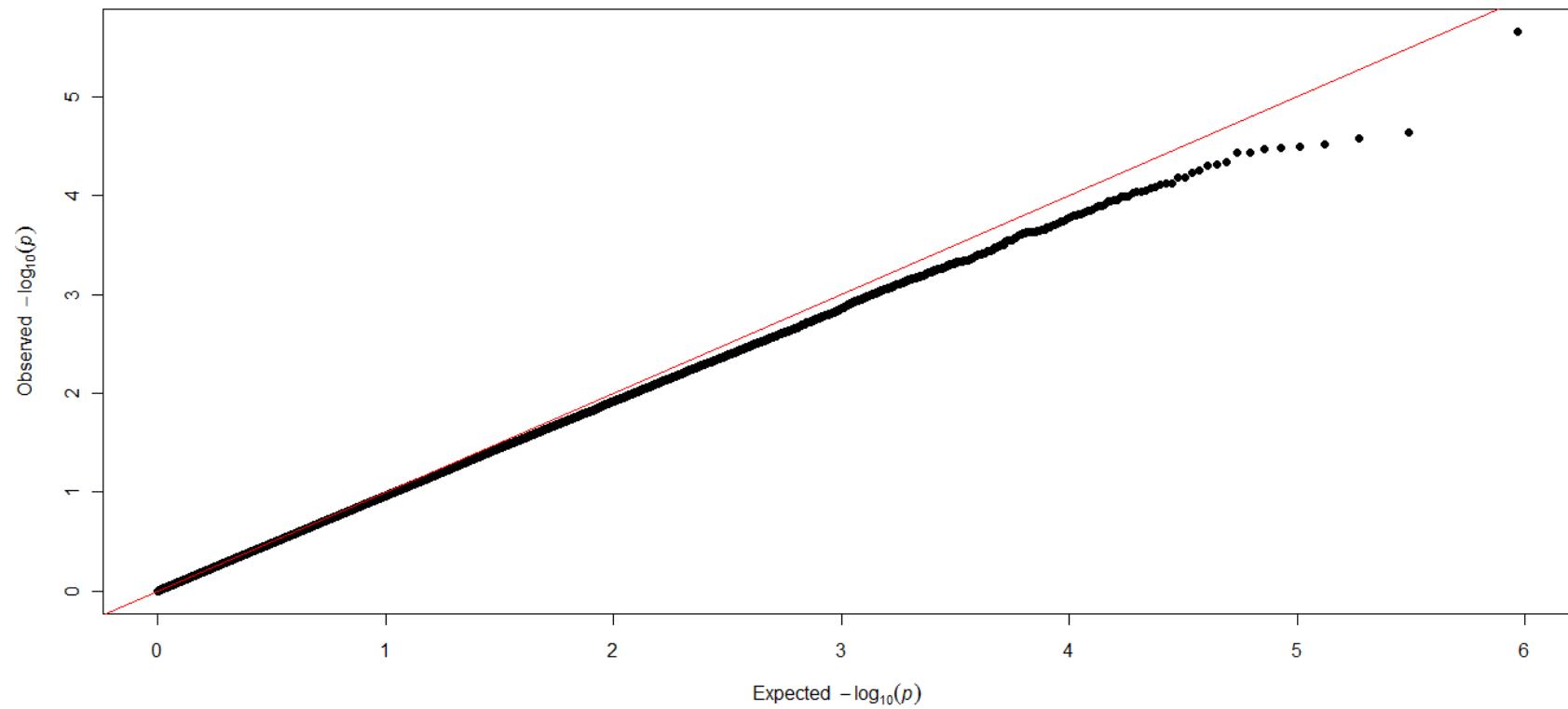
Panel D: Total number of HDL particles ($\lambda=1.1$)



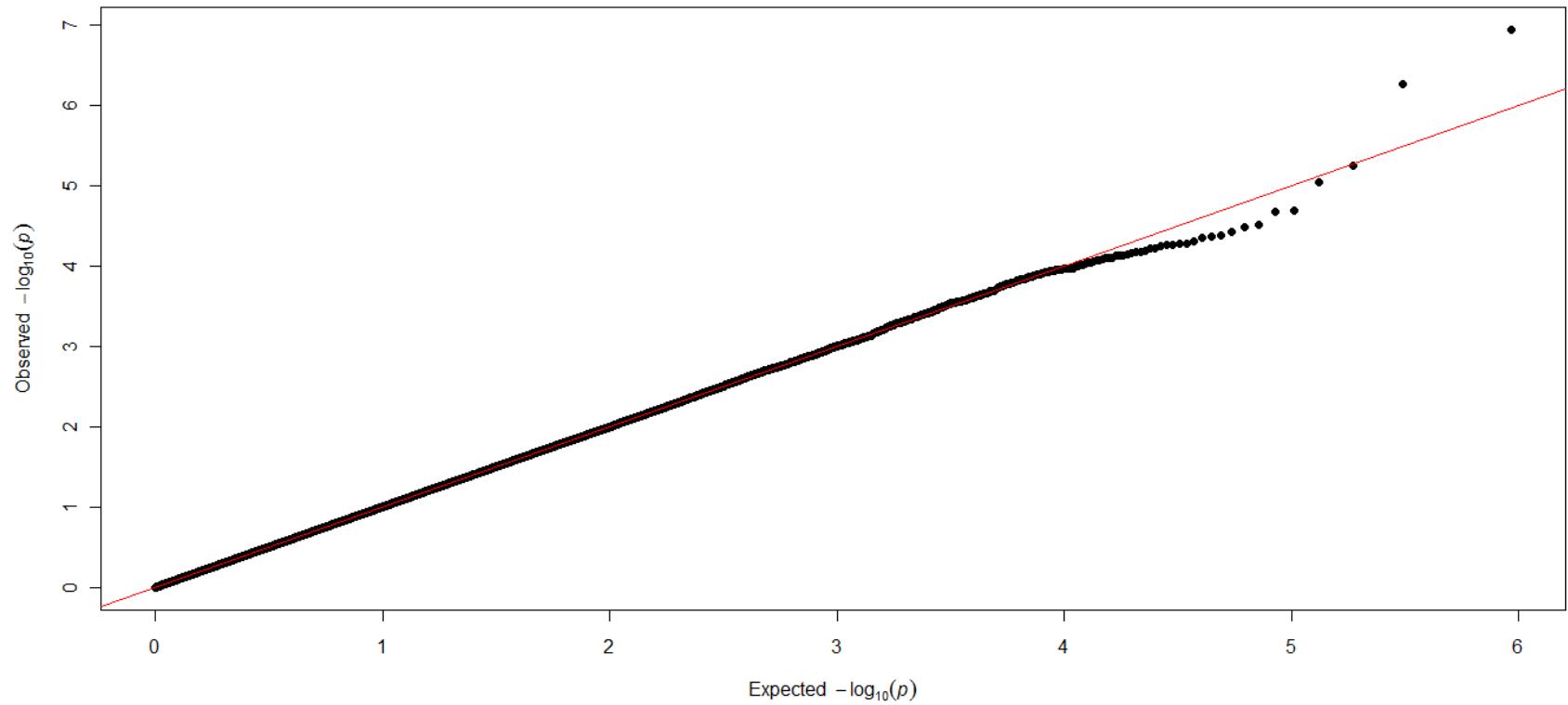
Panel E: Average HDL diameter ($\lambda=1.0$)



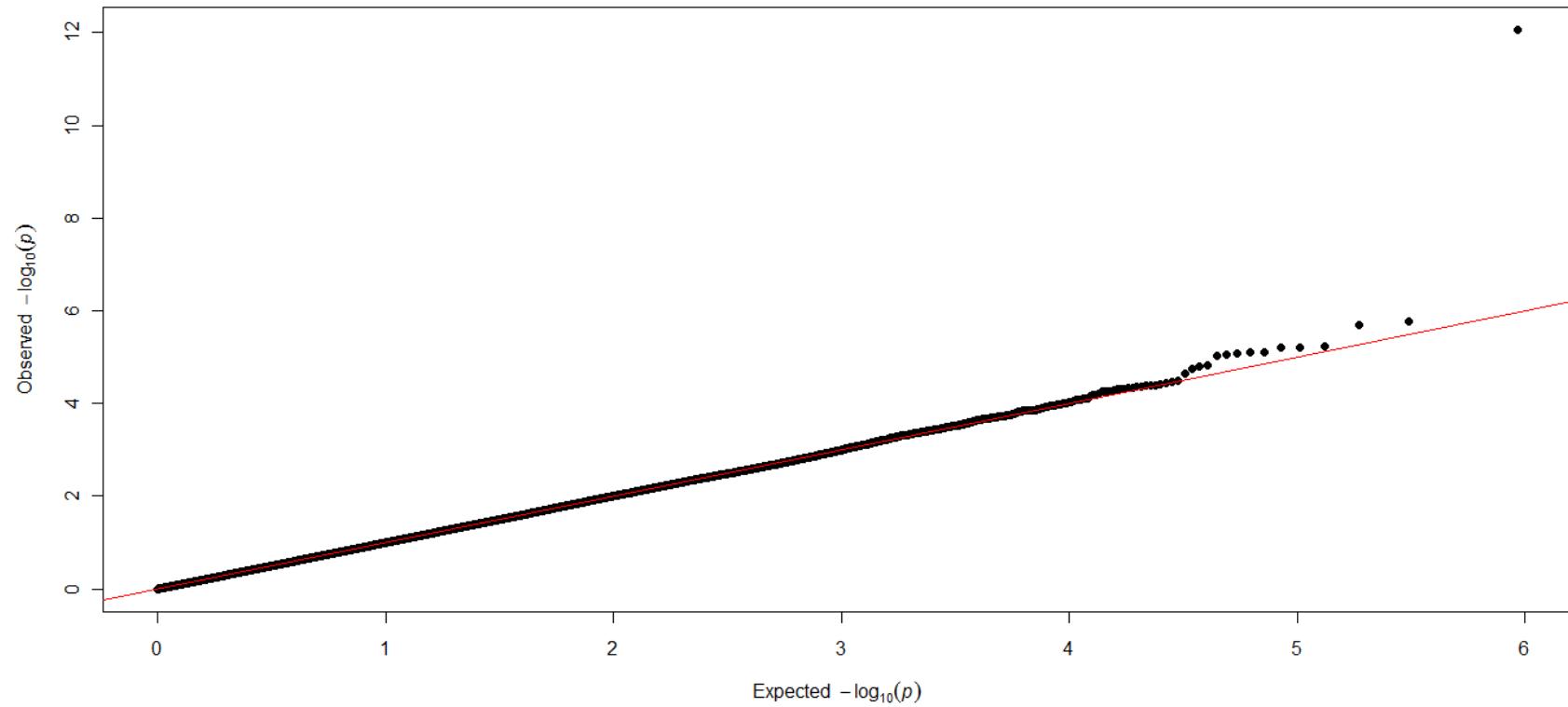
Panel F: Total number of IDL particles ($\lambda=1.0$)



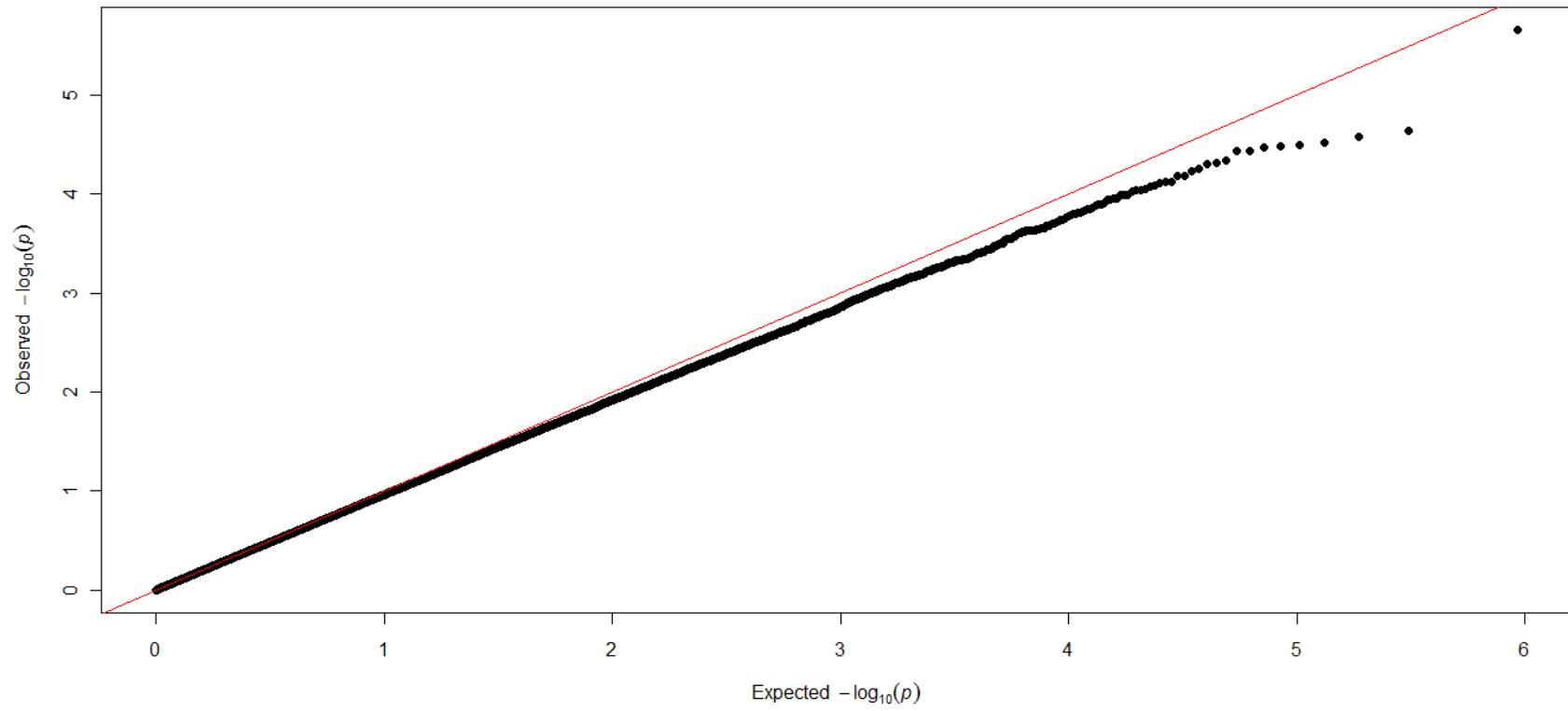
Panel G: Concentration of large LDL particles ($\lambda=1.0$)



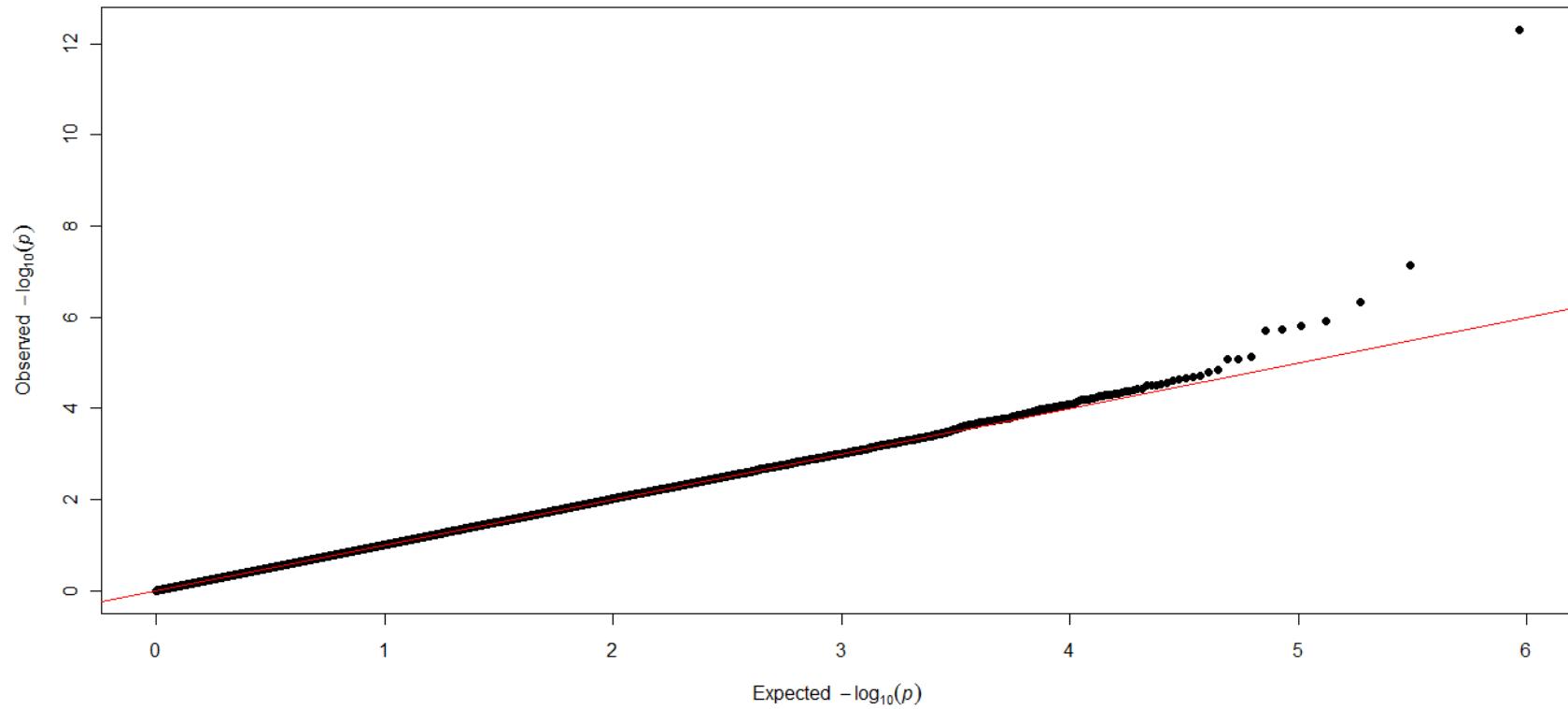
Panel H: Concentration of small LDL particles ($\lambda=1.0$)



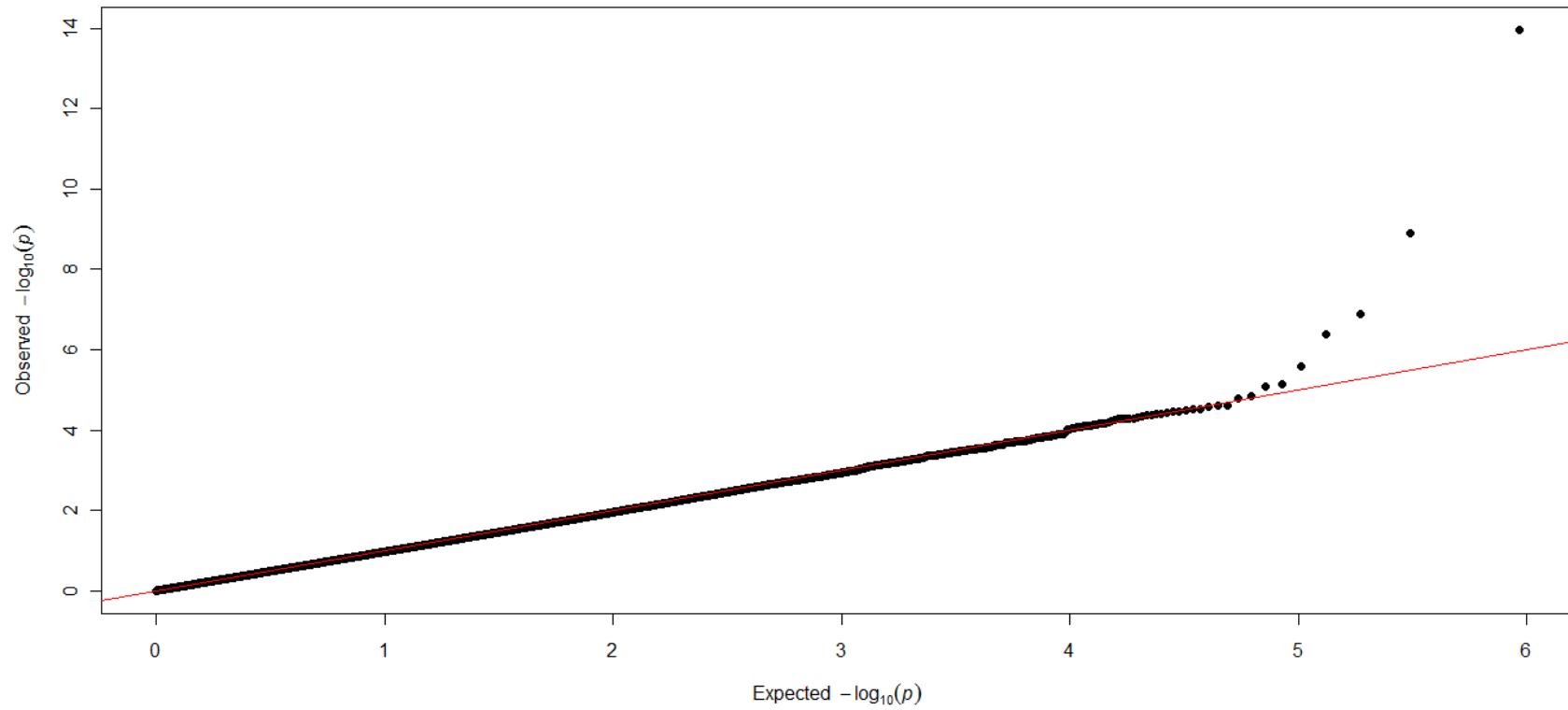
Panel I: Total number of LDL particles ($\lambda=1.0$)



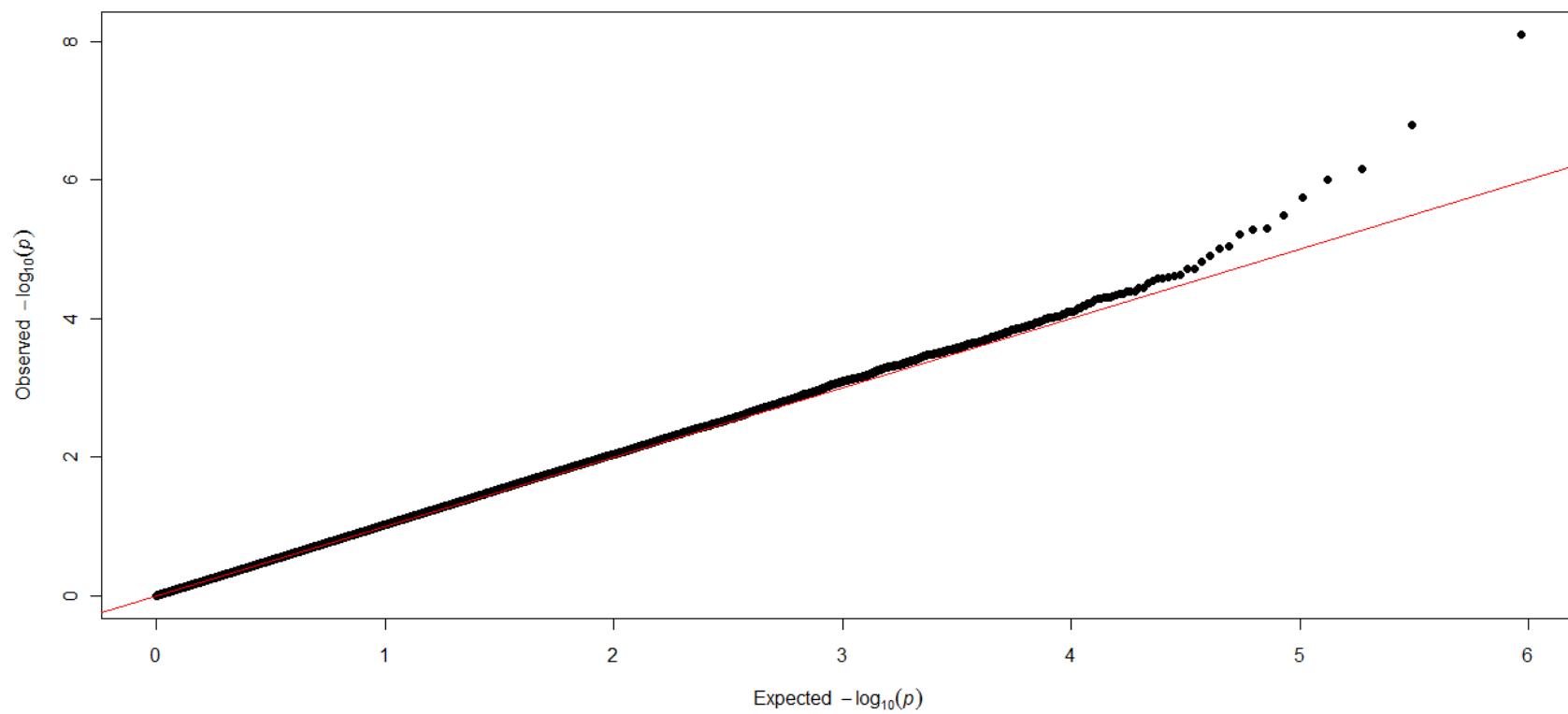
Panel J: Average LDL diameter ($\lambda=1.0$)



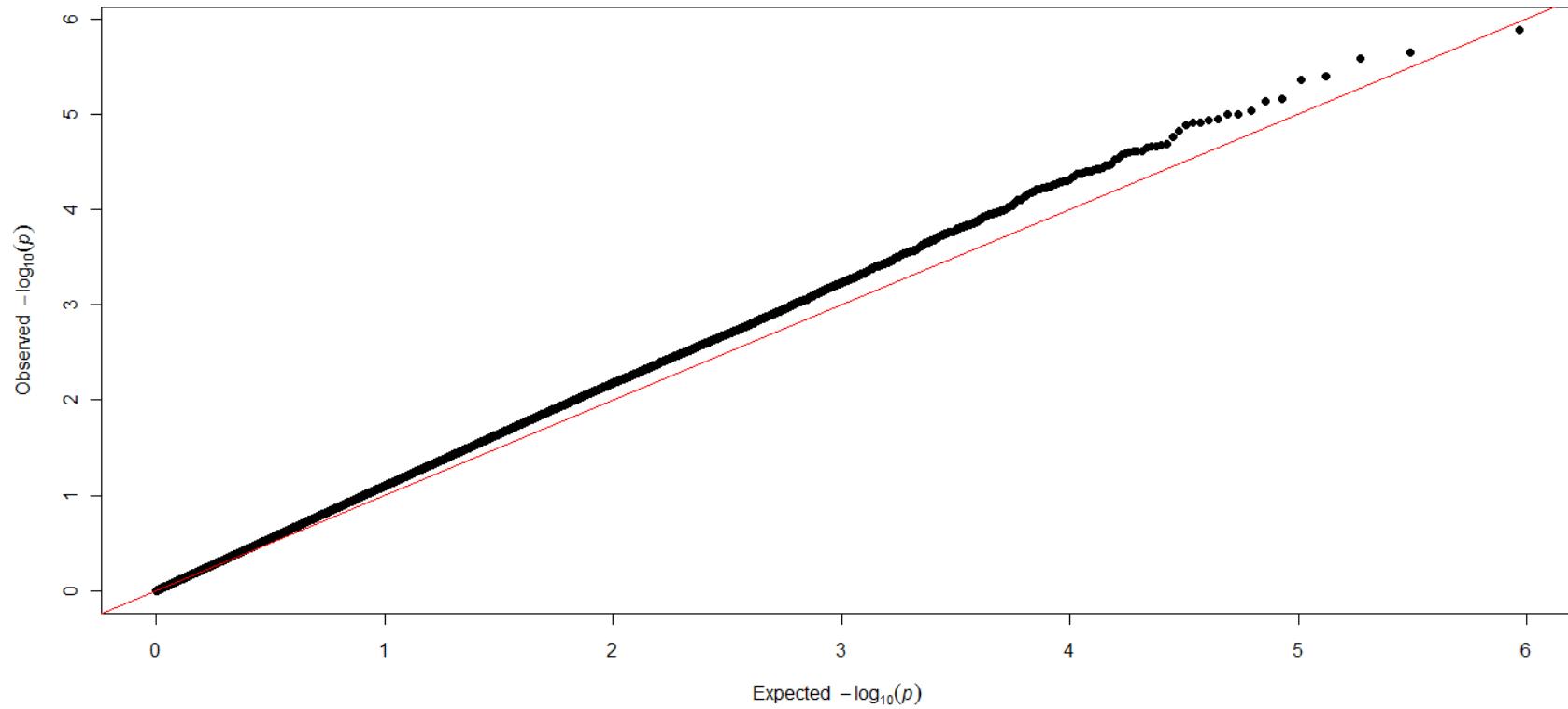
Panel K: Concentration of large VLDL particles ($\lambda=1.0$)



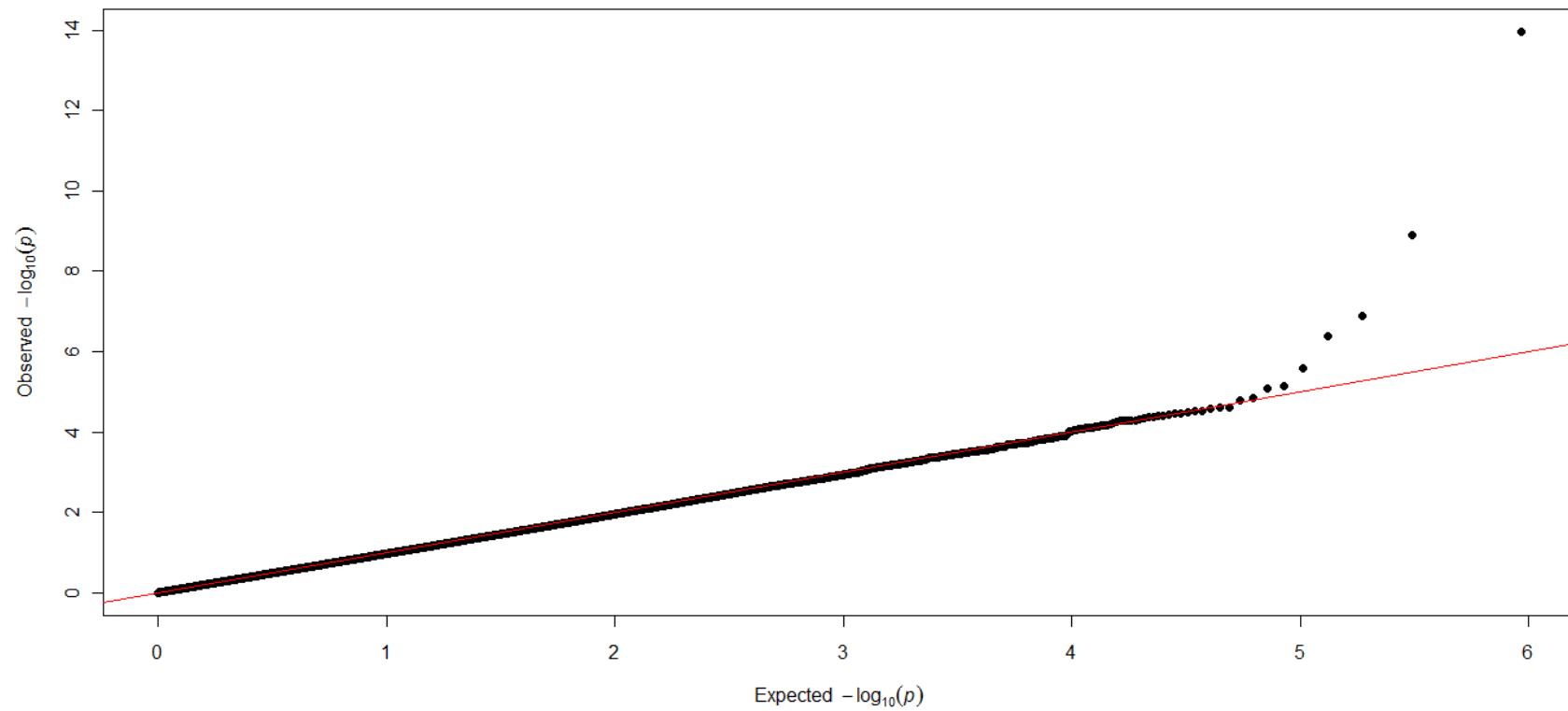
Panel L: Concentration of medium VLDL particles ($\lambda=1.0$)



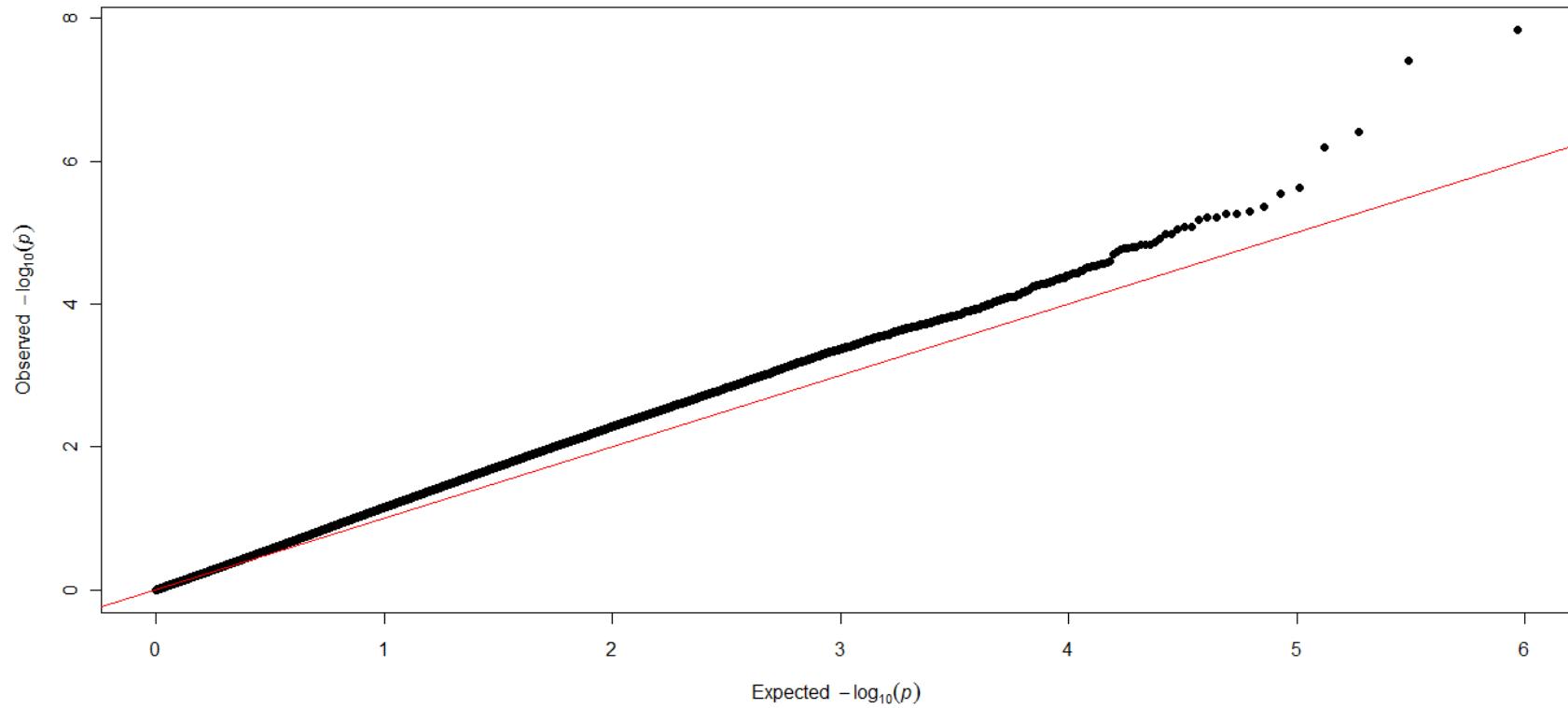
Panel M: Concentration of small VLDL particles ($\lambda=1.1$)



Panel N: Total number of VLDL particles ($\lambda=1.0$)

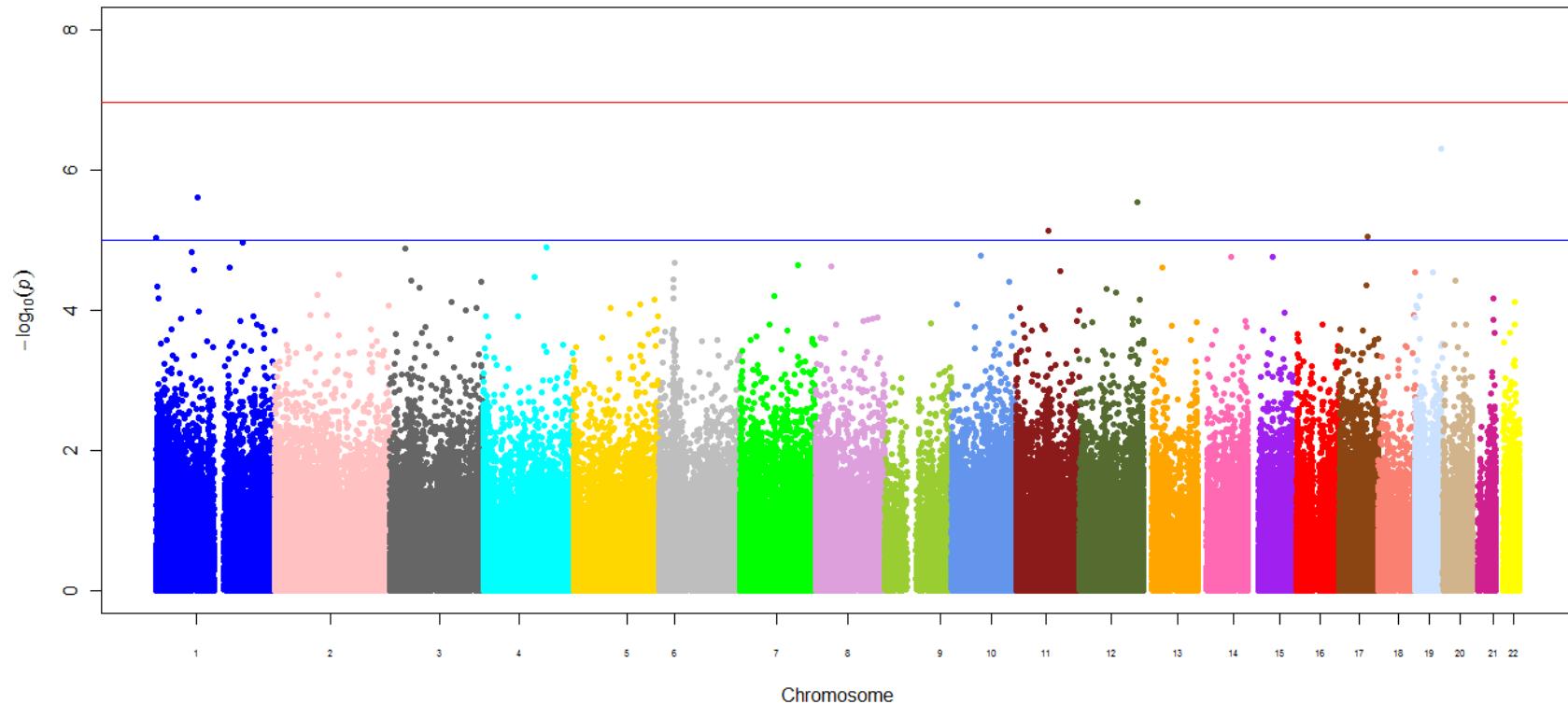


Panel O: Average VLDL diameter ($\lambda=1.2$)

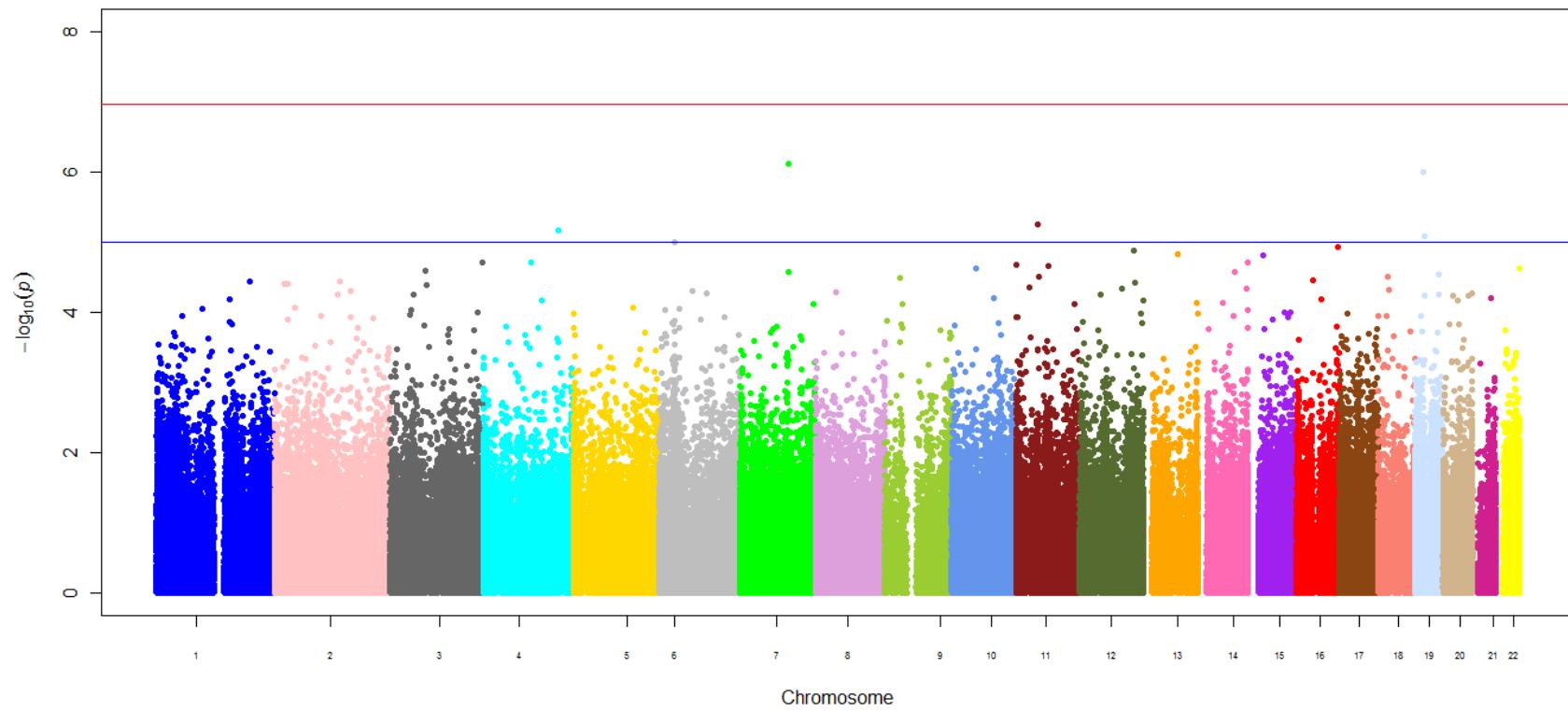


Supplementary Figure 2: Manhattan plots for the epigenome-wide analysis of methylation status at CpG sites with fasting lipoprotein parameters (discovery subsample, n=663).

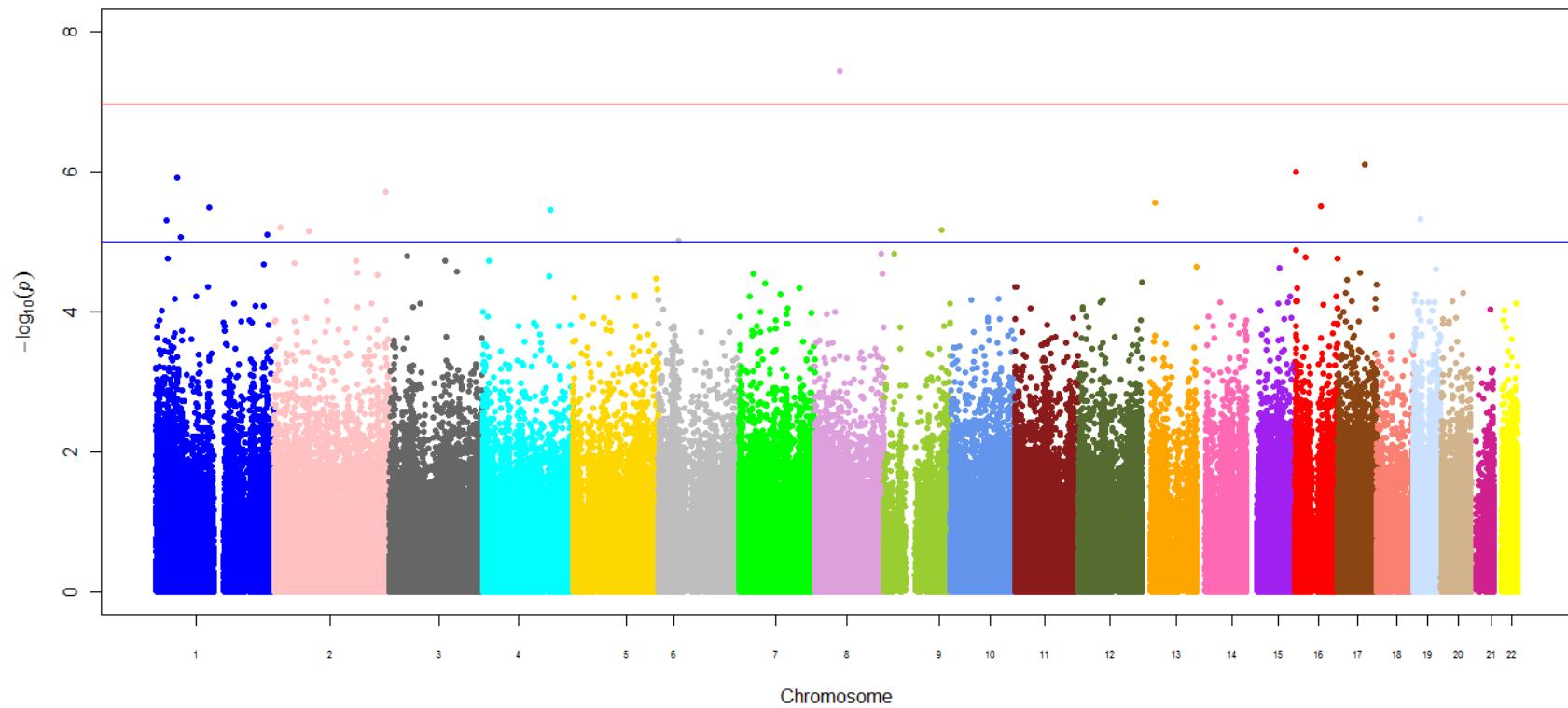
Panel A: Concentration of large HDL particles



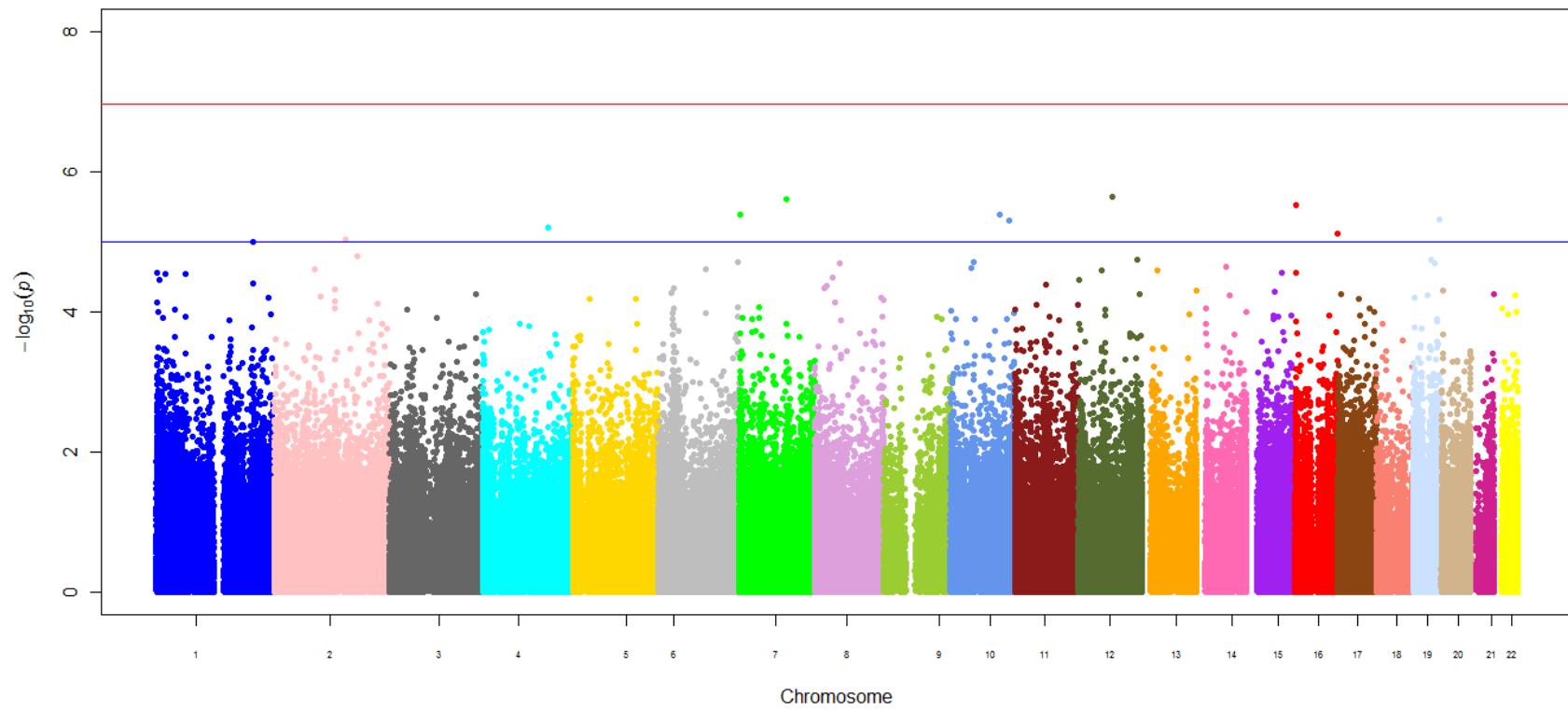
Panel B: Concentration of medium HDL particles



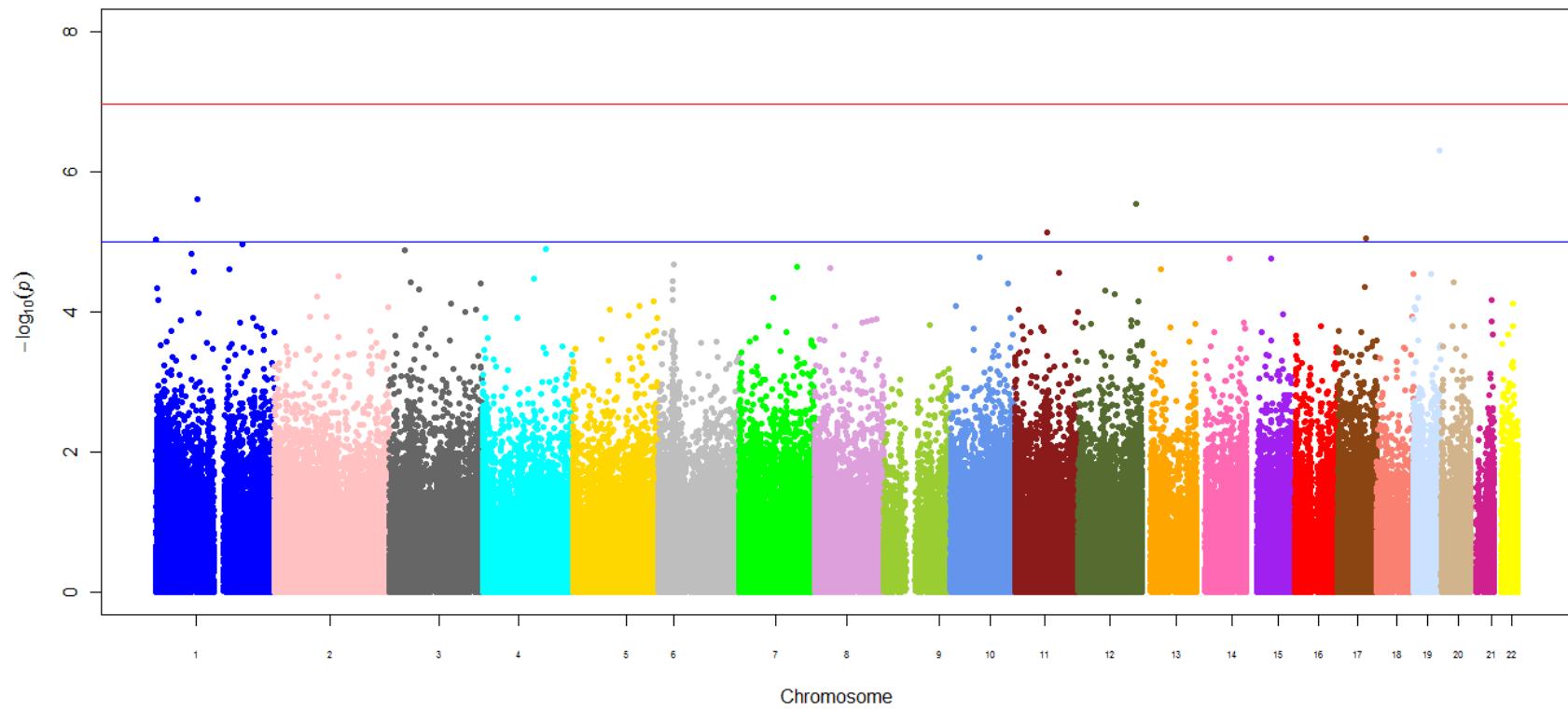
Panel C: Concentration of small HDL particles



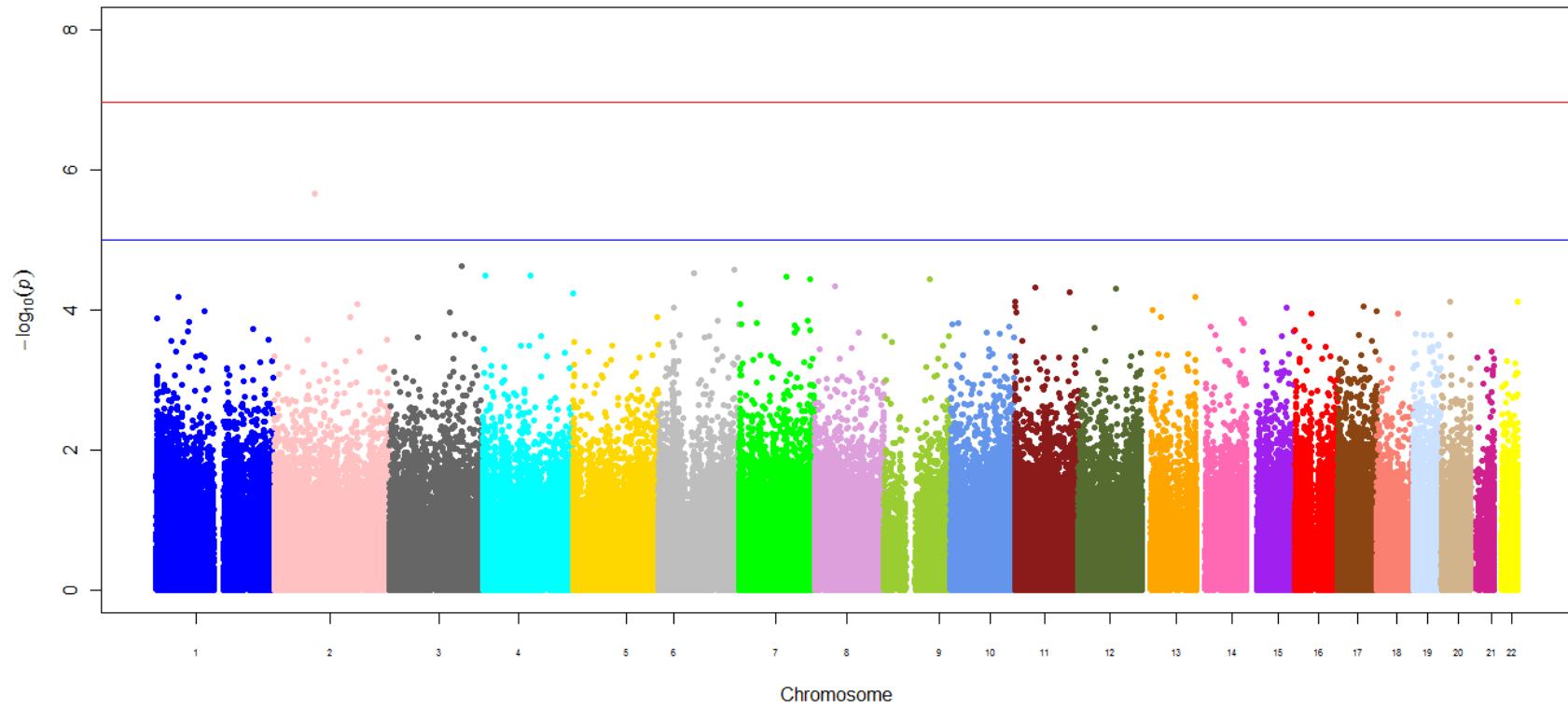
Panel D: Total number of HDL particles



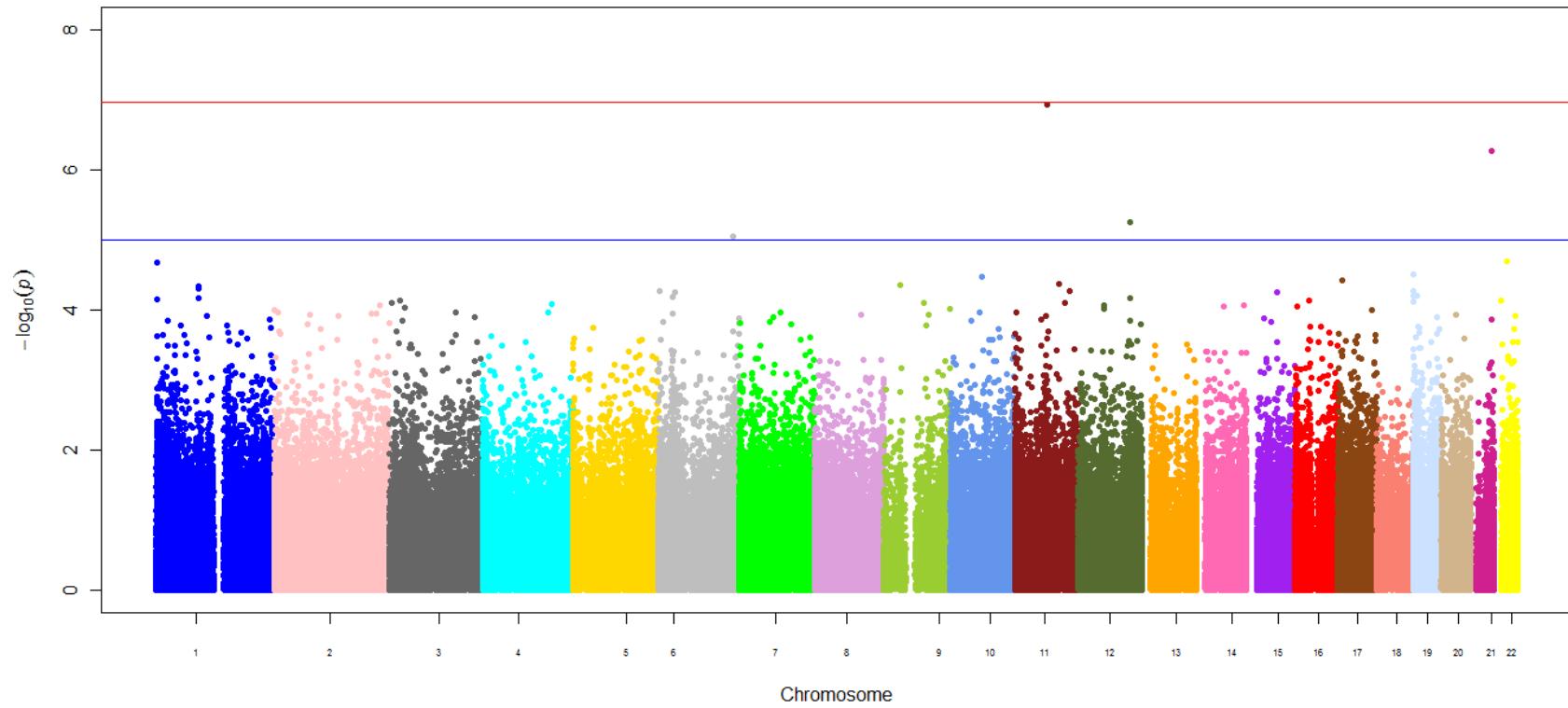
Panel E: Average HDL diameter



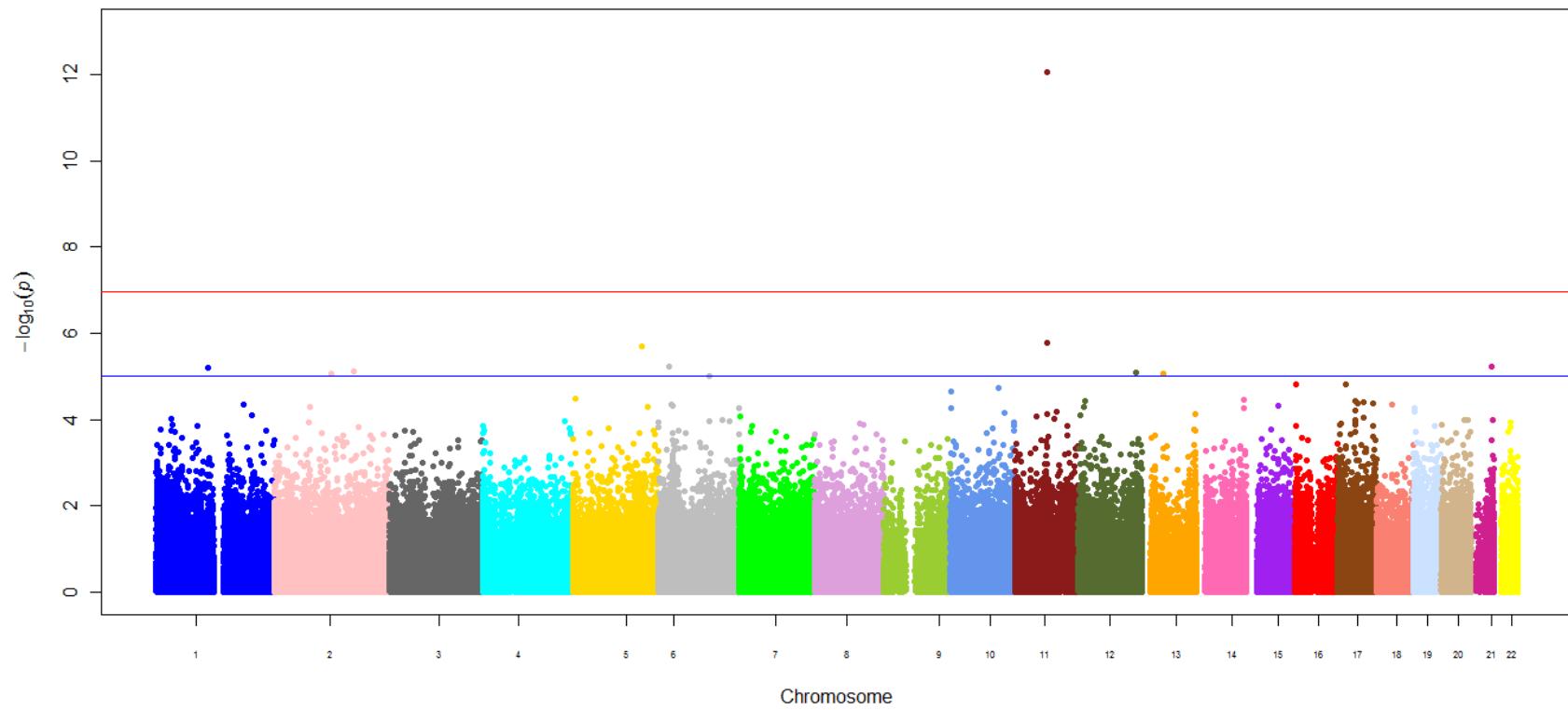
Panel F: Total number of IDL particles



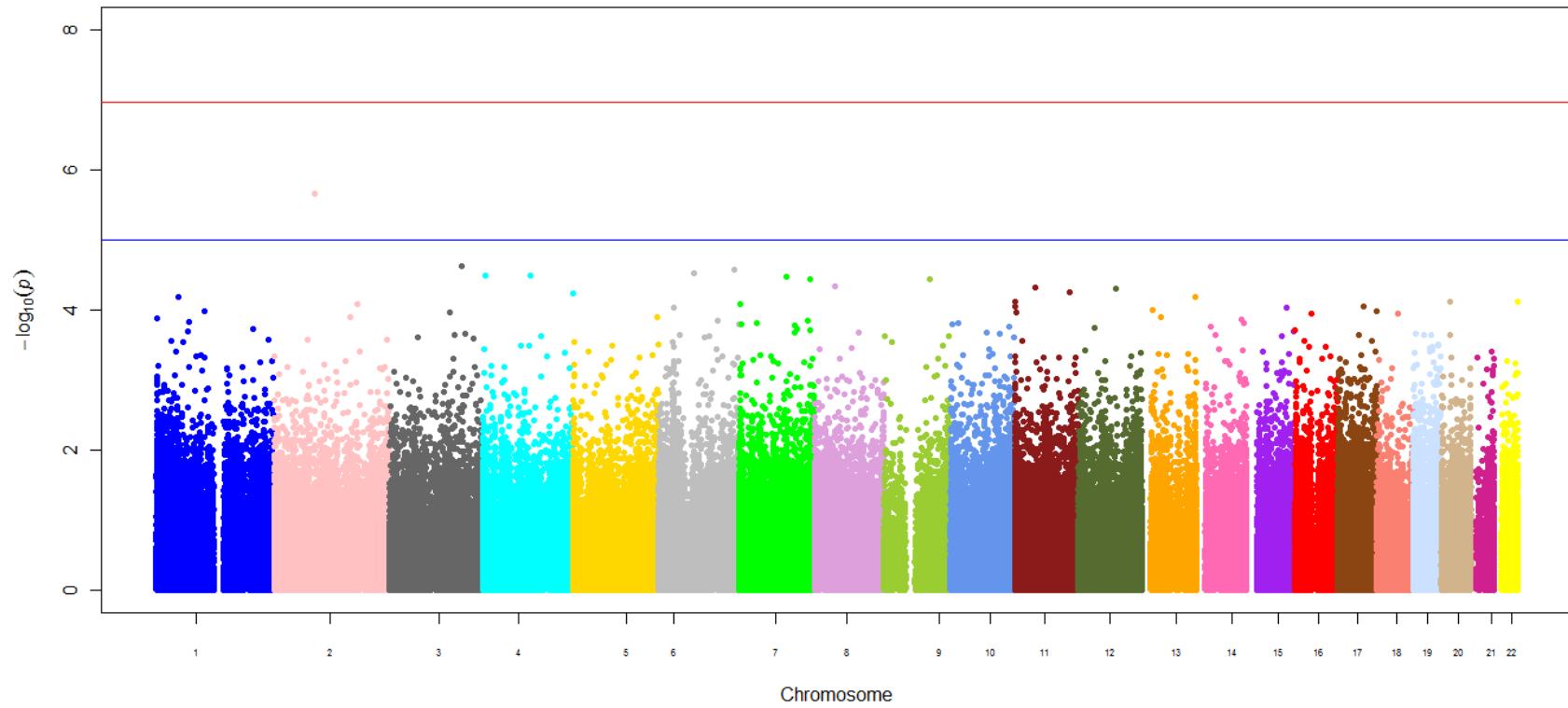
Panel G: Concentration of large LDL particles



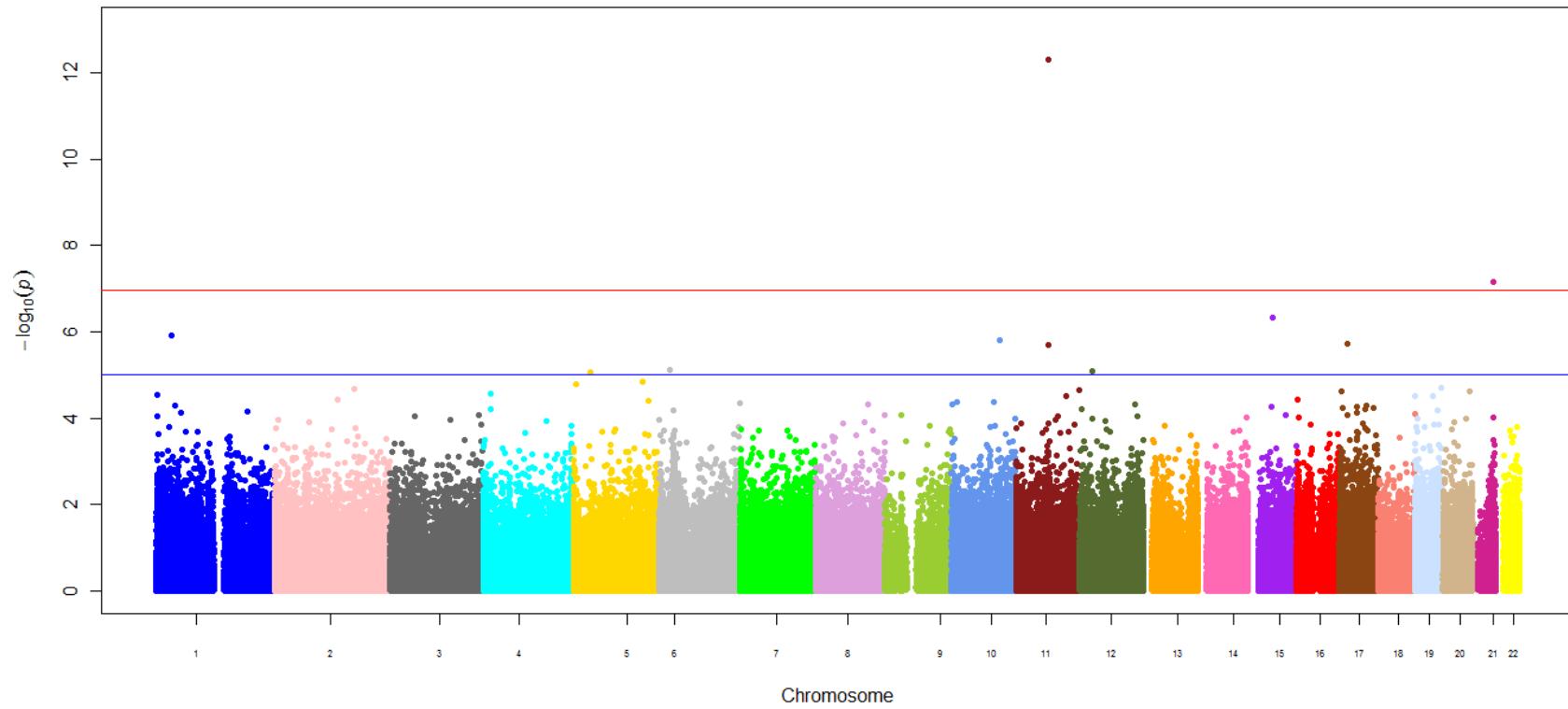
Panel H: Concentration of small LDL particles



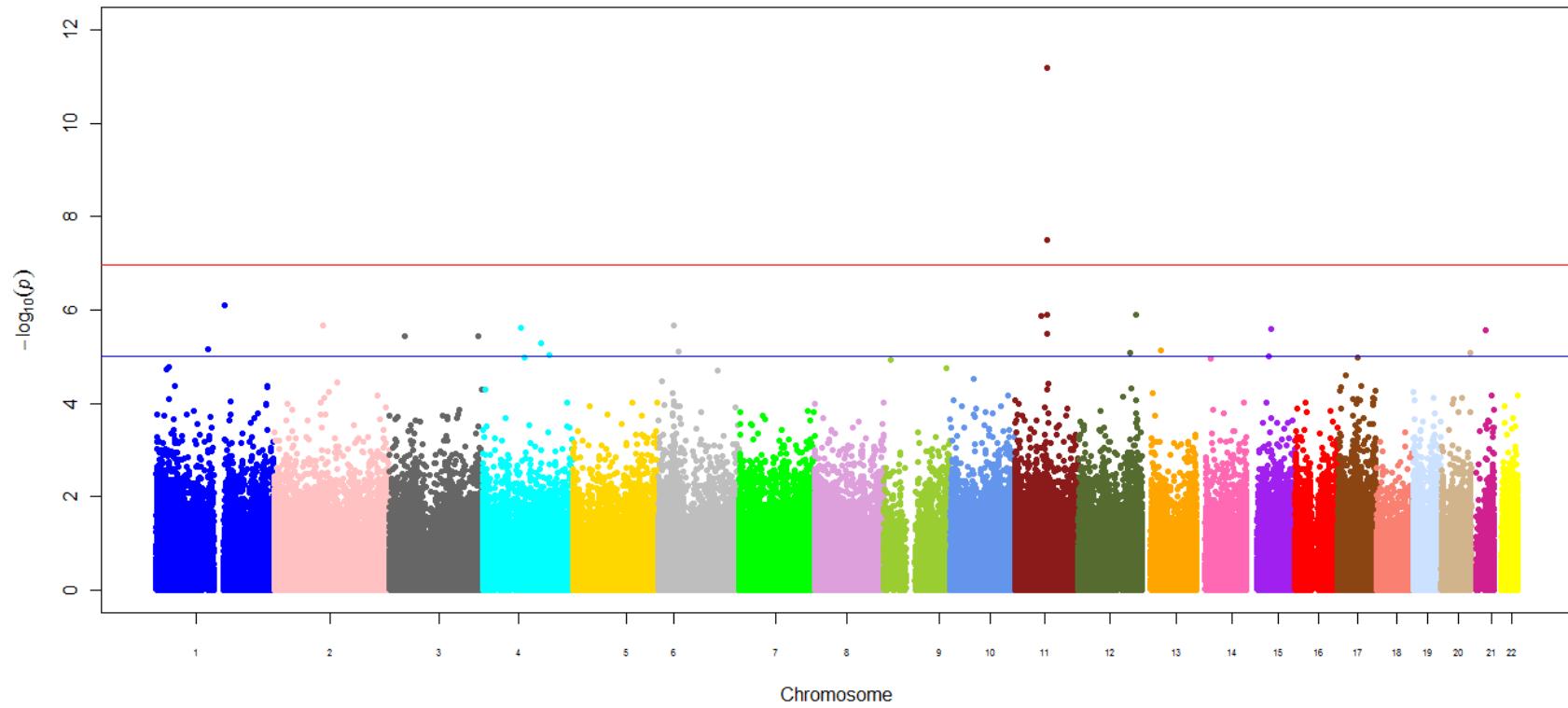
Panel I: Total number of LDL particles



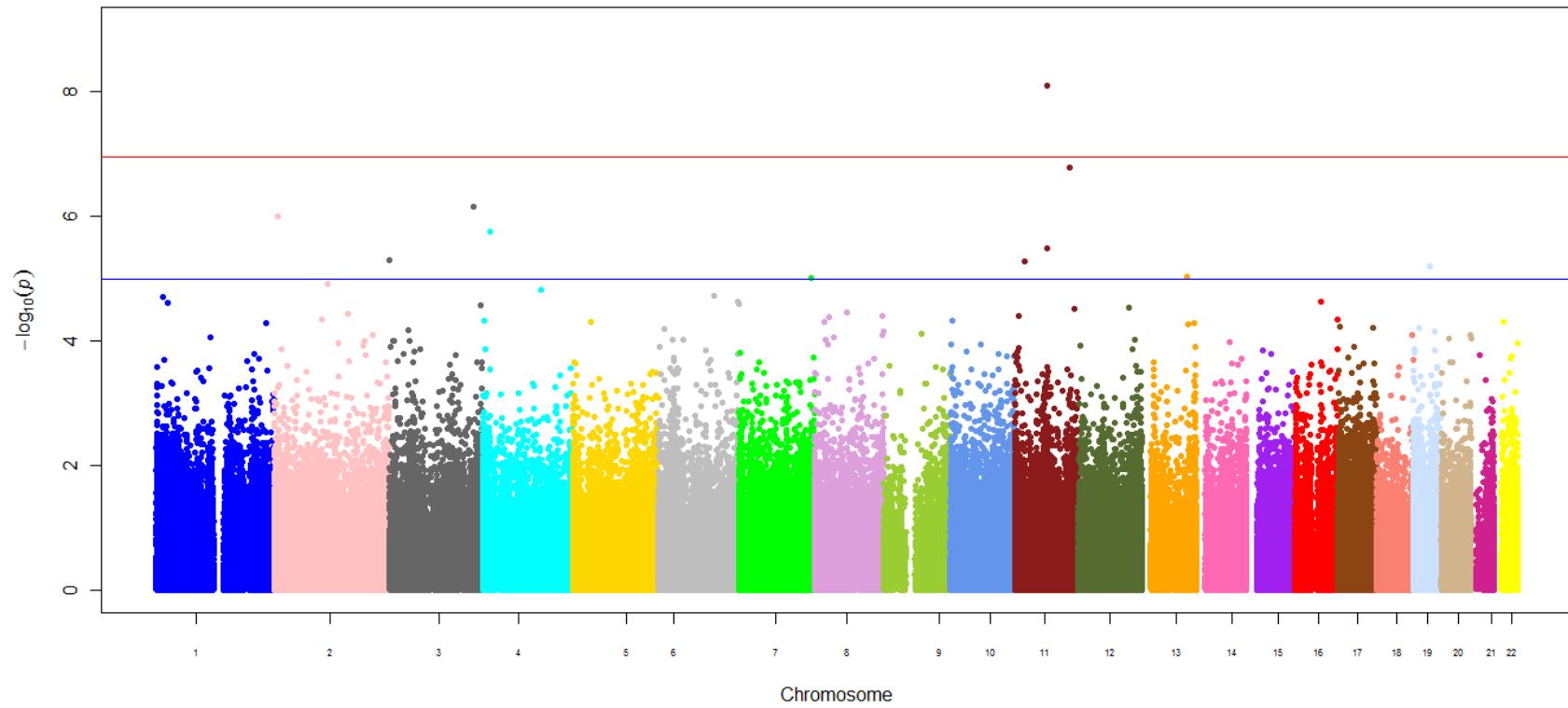
Panel J: Average LDL diameter



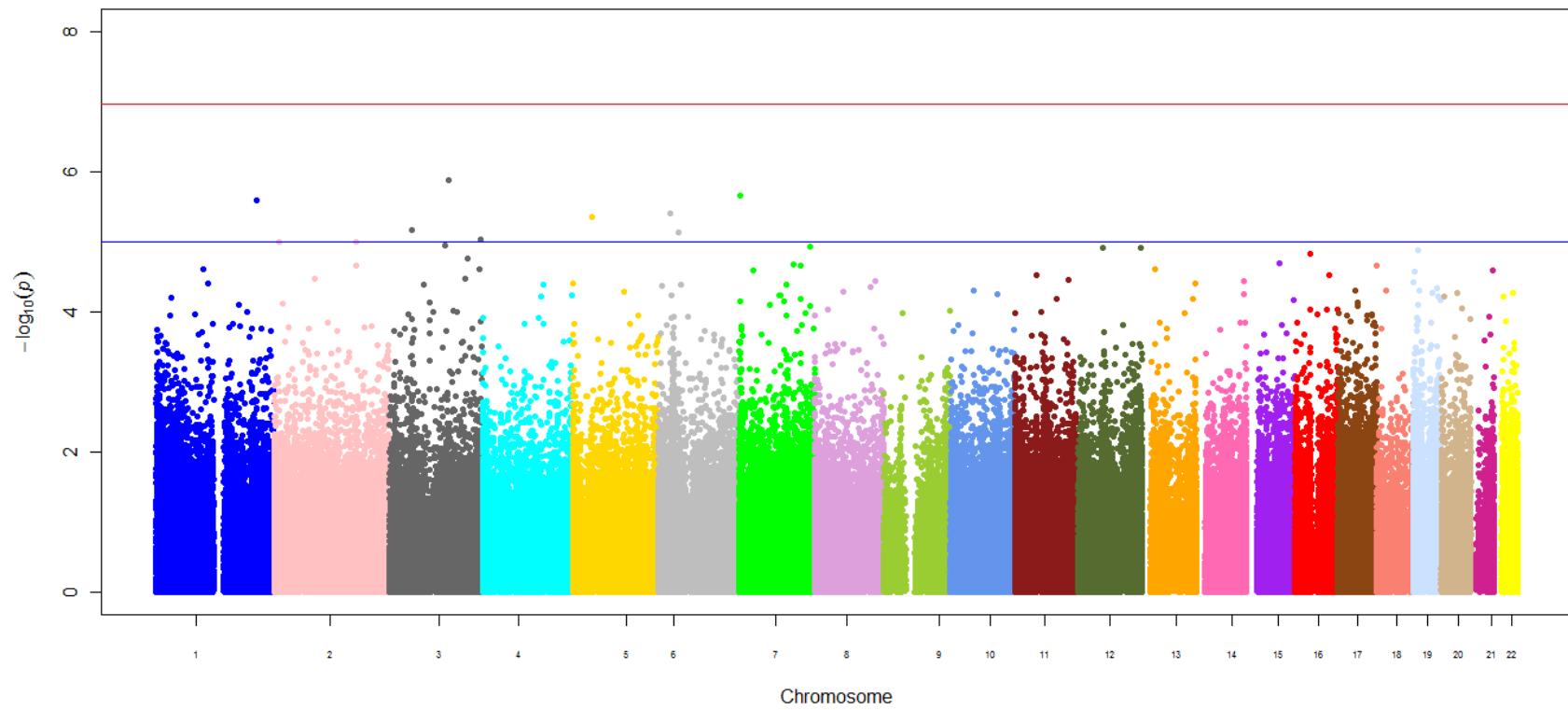
Panel K: Concentration of large VLDL particles



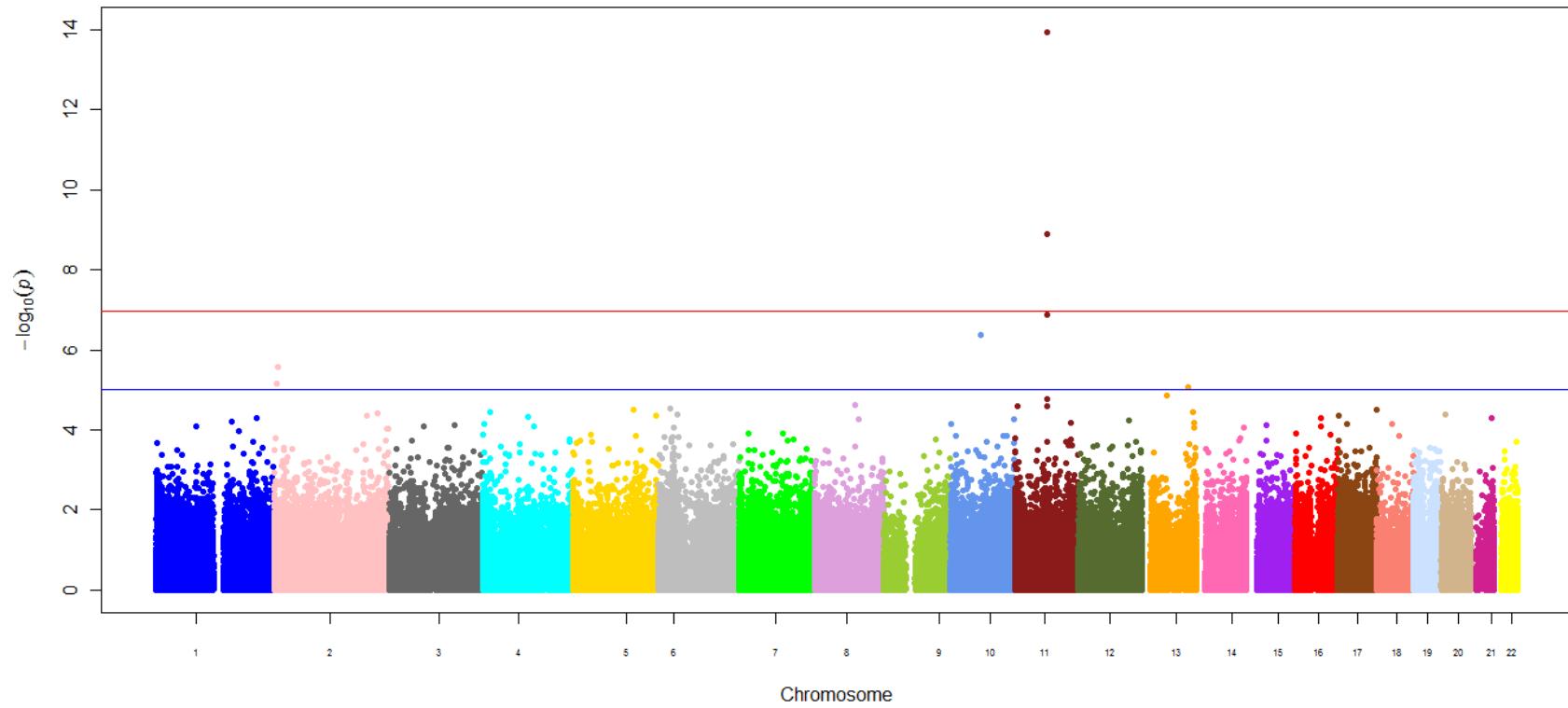
Panel L: Concentration of medium VLDL particles



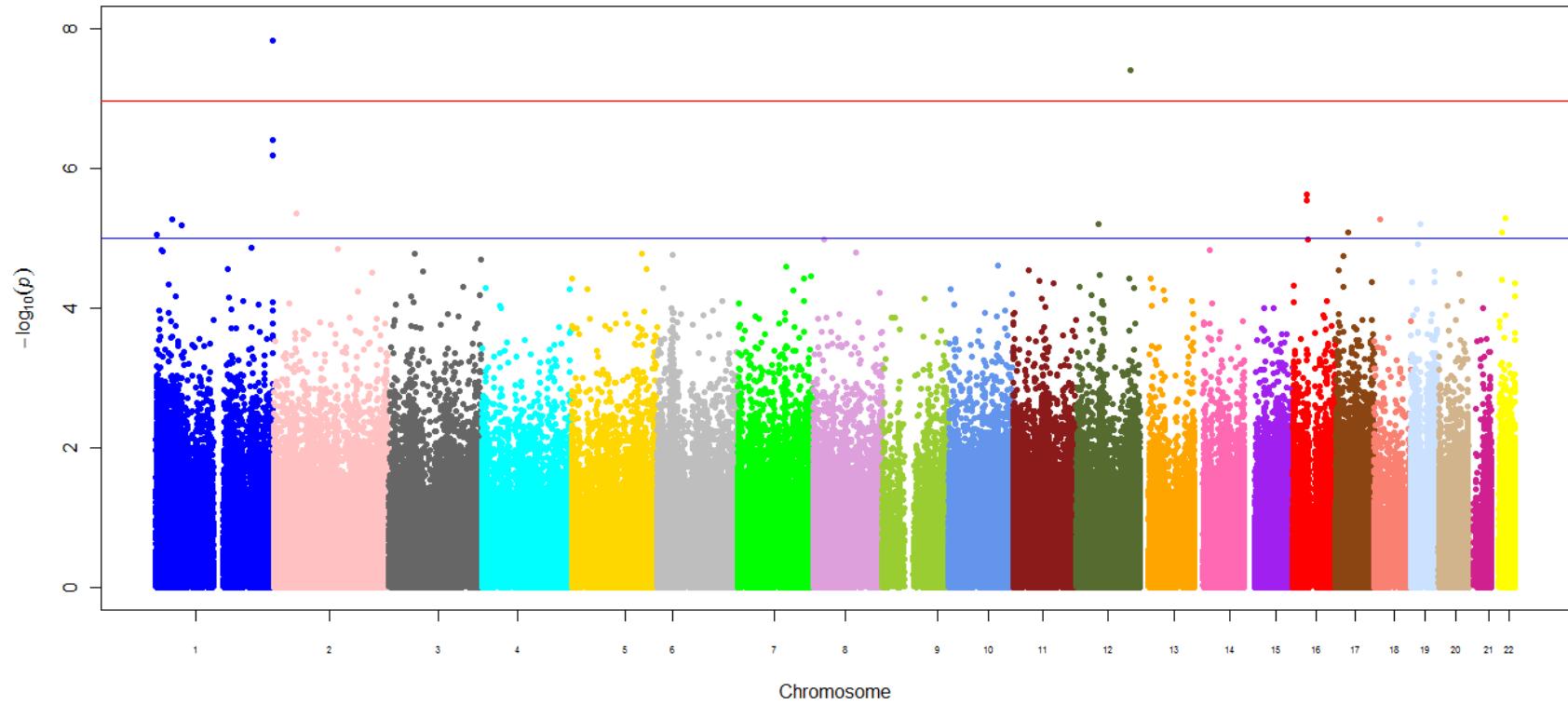
Panel M: Concentration of small VLDL particles



Panel N: Total number of VLDL particles

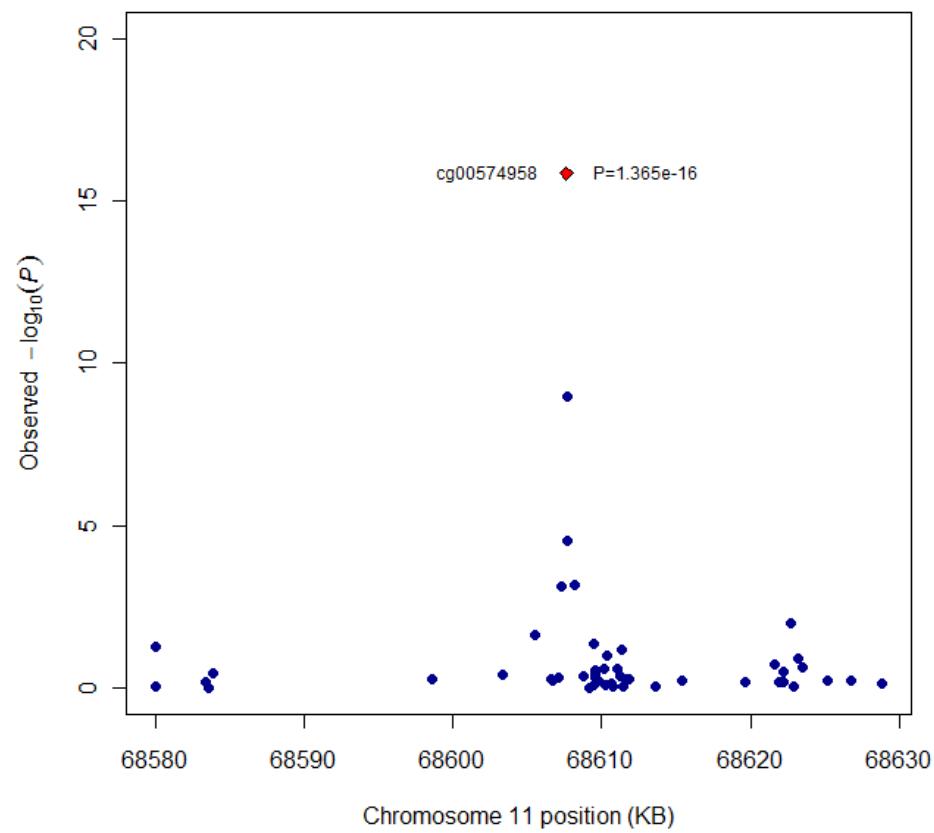


Panel O: Average VLDL diameter

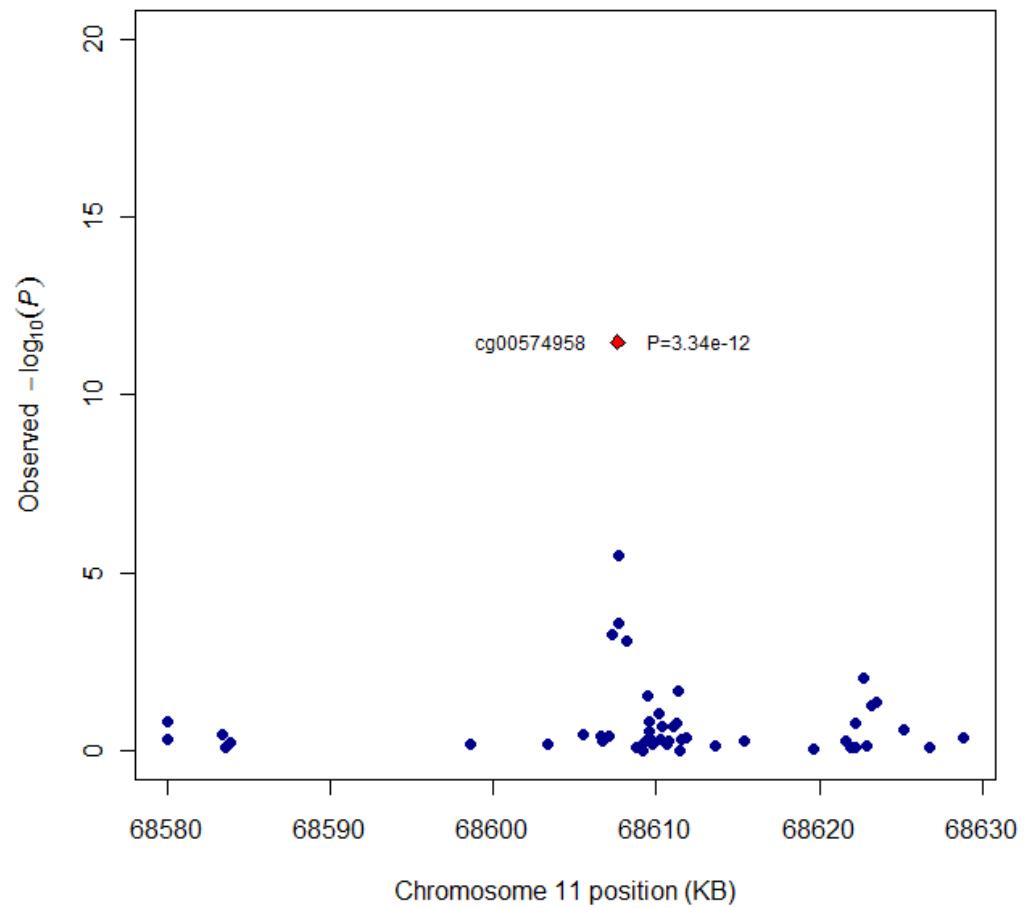


Supplementary Figure 3: Regional plots across the whole GOLDN sample (N=994) for the epigenome-wide analysis of methylation status at CpG sites with fasting lipoprotein parameters for significant CpG-phenotype associations

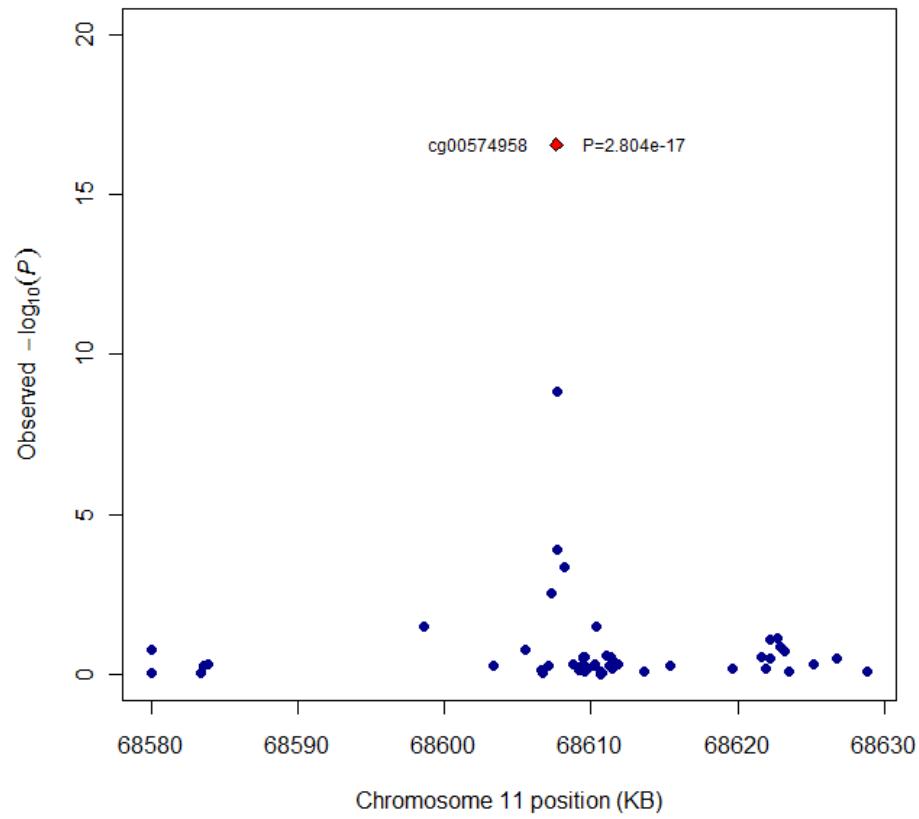
Panel A: Concentration of small LDL particles



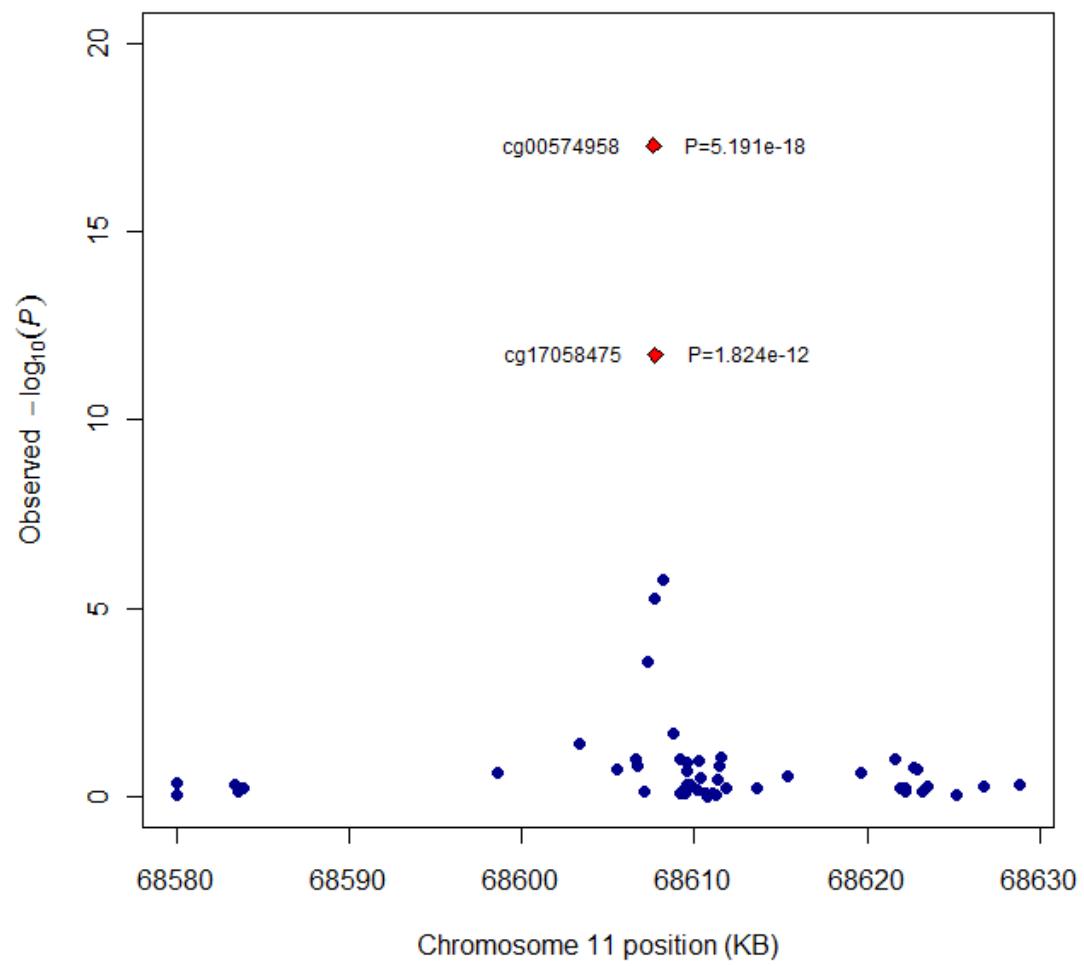
Panel B: Total number of LDL particles



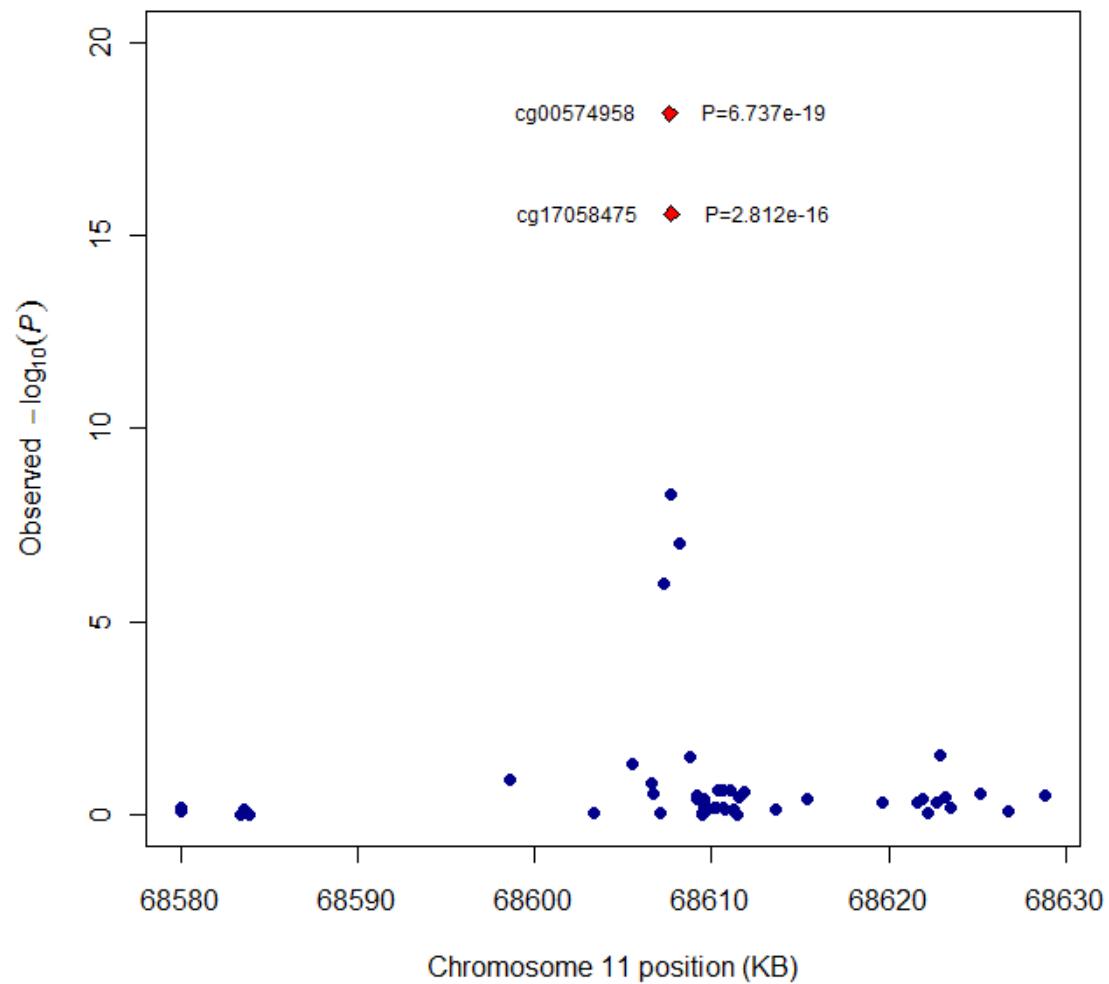
Panel C: Average LDL diameter



Panel D: Concentration of large VLDL particles



Panel E: Concentration of medium VDL particles



Panel F: Total number of VLDL particles

